GenCore version 5.1.3 Compugen Ltd

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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seq length: 2000000000
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(without alignments)
30.067 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIE

Bovine prion prote	AAY07999	20	42	100.0	55	10
Prion protein regi	AAR38035	14	26	100.0	55	9
Human prion protei	AAR38032	14	18	100.0	55	80
Ovine prion protei	AAR38029	14	18	100.0	55	7
Bovine prion prote	AAR38026	14	18	100.0	55	6
Prion protein, PrP	AAU11856	23	16	100.0	55	<sub>5</sub>
Prion protein, PrP	AAU11825	23	16	100.0	55	4
Octa-peptide motif	AAB84521	22	14	100.0	55	ω
Prion mimetic pept	ABB81629	23	11	100.0	55	2
Prion protein, PrP	AAU11824	23	8	100.0	55	1
Description	ID	DB	Query Match Length DB	Query	Score	Result No.

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errón brocern cerr	בסיים ליכור כ	protein	procern	rotoi:	doi:10	Rhesus monkey prio	o,	rion p		Human prion protei	Homo		Human prion protei	Human PrP prion pr					prion p	t prion prot	pithe pr	prion	e rbPrP	e prion	prion	e prion	acid	cid sequen	PrP	prp	prion	prion	prion	pr Pr	Peptide sequences

## ALIGNMENTS

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RESULT 1
AAU11824
Prion protein; Prp; ligand; octapeptide motif; scrapie; prion-associated disease; Creutzfeldt-Jakob disease; Gerstmann-Straussler-Scheinker disease; fatal familial insomnia; feline spongiform encephalopathy; bovine spongiform encephalopathy; transmissible mink encephalopathy; exotic ungulate encephalopathy;
         WPI; 2002-061944/08
                                                                        05-APR-2000; 2000US-0543188.
                                                                                                                                                                                  chronic wasting disease.
                                                                                                                                                                                                                                                                                                       AAU11824;
                             Hammond DJ,
                                                                                             05-APR-2001;
                                                                                                                   18-OCT-2001.
                                                                                                                                       WO200177687-A2
                                                                                                                                                             Mammalia.
                                                                                                                                                                                                                                                          Prion protein, PrP, octapeptide motif.
                                                                                                                                                                                                                                                                                 26-MAR-2002
                                                                                                                                                                                                                                                                                                                          AAU11824 standard; peptide; 8 AA.
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                                                   TECHNOLOGIES INC.
                             Wiltshire VR,
                                                                                           2001WO-US11150.
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                              Carbonell
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                             Η;
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                                                                                                                                                                                                  WPI;
  Example;
                                                          thermostable
                                                                           Inactivating transmissible spongiform encephalopathy (TSE) agent as Creutzfeldt-Jacob disease, scrapie, kuru or Gerstmann-Straussler-Scheinker syndrome involves exposing agent t
                                                                                                                                                                                                                                                          Raven NDH
                                                                                                                                                                                                                                                                                                              (MICR-)
                                                                                                                                                                                                                                                                                                                                                                     08-JAN-2001;
26-FEB-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 scrapie;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transmissible spongiform encephalopathy; prion protein; sterilisation; immunisation; Creutzfeldt-Jacob disease; kuru; fatal familial insomnia; Gerstmann-Straussler-Scheinker syndrome; chronic wasting disease; bovine spongiform encephalopathy; feline spongiform encephalopathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prion mimetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prion mimetic peptide SEQ ID NO:1.
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8; Conser
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  Page
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ilarity 100.
Conservative
                                                       proteolytic enzyme
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2001GB-0004696.
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  19;
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41pp;
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  English
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Pred. No. 7.8
D; Mismatches
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7.8e+05;
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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cc spongiform encephalopathy, scrapie, feline spongiform encephalopathy, cc chronic wasting disease or transmissible mink encephalopathy. (I) is cuseful for sterilising material contaminated with the TSE agent. A prion cd dimer is useful for examining a sample infected with or suspected to be infected by a prion protein, and for detecting prion infectivity, by cc detecting a prion dimer in the sample. A prion dimer is useful for cc producing (II), by immunising an animal with a prion dimer, obtaining its certract which contains (II), and isolating (II) from the extract. The cc extract which contains (II), and isolating (II) from the extract. The cc extract bind a prion dimer, and removing (II) from the preparation. (M1) cc and (I) are useful for inactivating TSE agents in potentially contaminated clinical waste and culled animal material. (M1) is useful for setrilising larger surface areas of apparatus, operating tables or ceven walls of rooms. The present sequence represents a prion minetic contaminated clinical waste and culled animal material.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a method (MI) for inactivating a transmissible spongiform encephalopathy (TSD) agent comprising exposing the TSE agent to a thermostable proteolytic enzyme. Also described:
(1) a composition (I) for inactivating a TSE agent, comprising a thermostable proteolytic enzyme; (2) an antibody (II) specific for a prion dimer which does not bind to a prion monomer; and (3) a purified prion dimer. (MI) is useful for inactivating a TSE agent such as a prion. A TSE agent is Croutzfeldt-Jacob disease or its variant, kuru, fatal familial insomnia, Gerstmann-Straussel-Scheinker syndrome, bovine
                                                                 Diagnosis of prion diseases, by treatment with proteinase detecting retention of octapeptide repeat motifs, including differentiation between prion strains \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                            Prion protein; subacute transmissible spongiform encephalopathy; ESST. Creutzfeld-Jakob disease; bovine spongiform encephalopathy; scrapie.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Octa-peptide motif repeated in human prion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB84521;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preparation of antibodies including dimer preferential antibodies
                                Example 1; Page 13; 51pp; French.
                                                                                                                                                WPI; 2001-408079/43
                                                                                                                                                                                Deslys J,
                                                                                                                                                                                                                                                           12-NOV-1999;
                                                                                                                                                                                                                                                                                              13-NOV-2000;
                                                                                                                                                                                                                                                                                                                                   17-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                       WO200135104-A1
                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB84521 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GWGQPHGG
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                                                                                                                                                                                                                       COMMISSARIAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity
8; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide;
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                                                                                                                                                                                    Grassi J;
                                                                                                                                                                                                                       ENERGIE ATOMIQUE.
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Pred. No. 0.
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0.027;
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The

present sequence represents an octa-peptide repeat motif of

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Best Local S
Matches
polypeptide containing the sequence GlyTyrGlyGlnProHisGlyGly (A) or an analogue that is the retro-inverso isomer of (A). The sequence A is an octapeptide motif from the prion protein (PrP). The ligands are identified by binding assays with the peptide (A) or peptides containing (A). The ligands are used for detecting prion proteins (or prions) in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of subacute transmissible spongiform encephalopathy (ESST) caused by a strain of unconventional transmissible agent. The method comprises detecting abnormal prion protein in a biological sample. The sample is treated with at least one proteinase K while retaining at least some of the octapeptide repeats in the prion protein, then treatment with a ligand for octapeptide repeats and detecting any formation of a complex. The method is used to diagnose ESST, particularly (new variant)
                                                                                                        Claim 1; Page 33; 47pp; English
                                                                                                                                                 New ligands for prion proteins, useful prions and for treating prion-associat
                                                                                                                                                                                                                          Hammond DJ,
                                                                                                                                                                                                                                                                                   05-APR-2000;
                                                                                                                                                                                                                                                                                                               05-APR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chronic wasting disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 feline spongiform encephalopathy; bovine spongiform encephalopathy; transmissible mink encephalopathy; exotic ungulate encephalopathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gerstmann-Straussler-Scheinker disease; fatal familial insomnia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prion protein,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Creutzfeld-Jakob diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prion protein. The specification describes a method for the diagnosis of subacute transmissible spongiform encenhalmatha recommendations.
                                                                                                                                                                                                                                                       (VITE-) VI TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                             18-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prion-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GWGQPHGG
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                                                                          invention relates to a ligand of less than 6 kD that binds
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8; Conserv
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                                                                                                                                                                                                                                                                                                               2001WO-US11150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prp; ligand; octapeptide motif;
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                                                                                                                                                 treating prion-associated
                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease; Creutzfeldt-Jakob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     octapeptide motif containing peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                             "Gly is acetylated"
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                                                                                                                                                                                                                          Carbonell
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Pred. No. 0.034;
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                                                                                                                                                                                                                          В,
                                                                                                                                                   for detection or removal or
ed diseases, recognize a spe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22;
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RESULT 5
AAU11856
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Best Local
polypeptide containing the sequence GlyTyrGlyGlnProHisGlyGly (A) or an analogue that is the retro-inverso isomer of (A). The sequence A is an octapeptide motif from the prion protein (PrP). The ligands are identified by binding assays with the peptide (A) or peptides containing (A). The ligands are used for detecting prion proteins (or prions) in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          scrapie, bovine or feline spongiform encephalopathy, transmissible mink or exotic ungulate encephalopathy, or chronic wasting disease. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prion-associated diseases, especially Creutzfeldt-Jakob diseases (in iatrogenic, new variant, familial or sporadic forms), but also Gerstmann-Straussler-Scheinker disease, fatal familial insomnia,
                                                                    The invention
                                                                                            Disclosure; Page 10;
                                                                                                                      octapeptide
                                                                                                                                                                          WPI; 2002-061944/08.
                                                                                                                                                                                                                            (VITE-) VI
                                                                                                                                                                                                                                                                              05-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chronic wasting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prion-associated disease; Creutzfeldt-Jakob disease;
Gerstmann-Straussler-Scheinker disease; fatal familial insomnia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prion protein, PrP, octapeptide motif containing peptide variant
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                                                                                                                                     prions
                                                                                                                                                                                                 Hammond DJ, Wiltshire VR, Carbonell
                                                                                                                                                                                                                                                                                                                                  WO200177687-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transmissible mink encephalopathy; exotic ungulate encephalopathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prion protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       feline spongiform encephalopathy;
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8; Conser
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                                                                                                                                 for treating
                                                                                                                                                                                                                            TECHNOLOGIES INC
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                                                                                                                     motif
                                                                                                                                              for prion proteins,
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                                                                  relates to a ligand of less than 6 kD that binds
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16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disease.
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                                                                                           47pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                   "Gly is acetylated"
                                                                                                                                  prion-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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Pred. No.
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                                                                                                                                                useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bovine spongiform encephalopathy;
                                                                                                                                                                                                 70,
                                                                                                                                                for
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0.038;
                                                                                                                                    diseases,
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                                                                                                                                             detection or removal or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             scrapie;
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RESULT 6
AAR38026
ID AAR39
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Best Local S
Matches 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             biological or environmental samples, e.g. for diagnosis, also for removing them from samples, for treating or retarding development of prion-associated diseases, especially Creutzfeldt-Jakob diseases (in latrogenic, new variant, familial or sporadic forms), but also Gerstmann-Straussler-Scheinker disease, fatal familial insomnia,
(PROT-) PROTEUS MOLECULAR DESIGN
                    03-DEC-1991;
10-JUL-1992;
                                                   03-DEC-1992;
                                                                          10-JUN-1993
                                                                                                                               Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                     human; sheep;
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nes 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                         prion; protein; region; frame shift; repeat; mutation;
                                                                                                                                                                                                                                                                                                                                                                                        subfragment; antibody; treatment; spongiform encephalopathy;
sep; cattle; cellular binding; aggregation; mammal; scrapie;
stem; PrPsc; ratio-inverso peptide; enzymatic degradation;
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ilarity 100.0%;
Conservative (
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RESULT 7
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            Misc-difference
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8; Conserv
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                                                                                                                                                                                                                                                                   subfragment; antibody; treatment; spongiform encephalopathy; eep; cattle; cellular binding; aggregation; mammal; scrapie; stem; PrPsc; ratio-inverso peptide; enzymatic degradation;
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RESULT 8
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                                  Misc-difference
                                                                                          Misc-difference
                                                                                                                                                                                                                                                                    human; sheep; cattle;
immune system; PrPsc;
                                                                                                                                                                                                                                                                                                                                                           Antigen; prion; protein; region;
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AAR38035

AAR38035 standard;

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AAR38035; 14-OCT-1993

(first entry)

Prion protein region E #2

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                                                                                                                                                                                                                                                                                                                             New polypeptide(s) contg. antigenic site of prion protein - useful for treatment and diagnosis of mammalian encephalopathies e.g. Creutzfeld-Jacob disease and kuru
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Misc-difference 16
                                                                                               Sequence
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Misc-difference 15
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Misc-difference 5
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                      1 GWGQPHGG 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequences given in AAR38025-36 represent polypeptides derived from an antigenic site, region E, of a prion protein. Prion proteins comprise six regions of interest (A-F), and two related frame shift peptides sequences caused by a repeating section in region E having a nucleic acid coding sequence frame shift mutation of +1 (FSa) or -1 (FSb) (see also AAR38037-38). These peptides and antibodies raised against these may be used to treat or prevent spongiform encephalopathy in humans, sheep or cattle. They can be used to block cellular binding and aggregation of prion proteins and to stimulate the mammalian immune system. These peptides may be used to distinguish between the normal form of prion protein (PPPc) and the scrapie-associated form (PPSc). These peptides may include rare or synthetic amino acids or a ratio-inverse peptide modification to improve resistance to enzymatic
                       DE19745443-A1
                                                                               Prion prote detection;
                                                                                                                           Bovine prion protein derived peptide III.
                                                                                                                                                        08-JUL-1999
                                                                                                                                                                                                                    AAY07999 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 24; Page 71; 82pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e.g. Creutzfeld-Jacob disease and kuru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polypeptide(s) contg. antigenic site of prion protein - useful for treatment and diagnosis of mammalian encephalopathies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1993-196994/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fishleigh RV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-DEC-1991;
10-JUL-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09311155-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antigen; prion; protein; region; frame shift; repeat; mutation; PrPc; FSa; FSb; subfragment; antibody; treatment; spongiform encephalopathy; buman; sheep; cattle; cellular binding; aggregation; mammal; scrapie; immune system; PrPsc; ratio-inverso peptide; enzymatic degradation;
                                                   Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                               degradation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PROT-) PROTEUS MOLECULAR DESIGN LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       resistance.
                                                                                                                                                                                                                                                                                             7
                                                                                                                                                                                                                                                                                                                                                     Local Similarity
es 8; Conserv
                                                                                                                                                                                                                                                                                                                         1 GWGQPHGG
                                                                                                                                                                                                                                                                                           protein; PrP
tion; bovine;
                                                                                                                                                                                                                                                                                                                                                                                                                  26
                                                                                                                                                                                                                                                                                                                                                   100.0%;
ilarity 100.0%;
Conservative (
                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                             14
                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                  Ą,
                                                                                             PrP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91GB-0025747.
92GB-0014663.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92WO-GB02246
                                                                                                                                                                                                                  protein; 42
                                                                                 murine
                                                                                               human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Robson B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
                                                                                             polyclonal antiserum;
                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                     Score 55; DE Pred. No. 0.0
                                                                                                                                                                                                                    Ą
                                                                                                                                                                                                                                                                                                                                                                     0.06;
                                                                                                                                                                                                                                                                                                                                                                                   DB 14;
                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                   Length 26
                                                                                               immunoassay;
                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                      0;
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RESULT 11
AAW70280
В
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Best Local
        01-MAY-1997;
06-FEB-1997;
24-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antiserum against a human or animal prion protein (PrF) which can be used in immunoassays for detecting PrF's. The method comprises (a) selecting a polypeptide that has a length of at least 10 amino acids and has an amino acid sequence at least 70% homologous to that of human, bovine or murine PrF in a region of at least 10 consecutive amino acids (b) binding a metal to the polypeptide by reaction with a metal compound and (c) injecting the metal-containing polypeptide into a host animal, optionally together with adjuvants, to induce production of a polyclonal
                                                        06-FEB-1998;
                                                                                                                                                 Region
                                                                                                                                                                                               Key
                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                   06-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                AAW70280 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel process for producing a polyclonal antiserum against a human or animal prion protein (PrP) which can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 4; 12pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Diagnostic polyclonal antiserum specific for prion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kiselev OI, Mesmer AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-OCT-1997;
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                                                                              13-AUG-1998
                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                    Spinal cord;
                                                                                                                                                                                                                                                                                         Peptide sequences used to raise antibodies against prion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HERZ/) HERZOG-MESMER A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-APR-1999
                                                                                                     WO9835236-A2
                                                                                                                                                                                                                                            immunological
                                                                                                                                                                                                                                                       3SE; scrapie;
                                                                                                                                                                                                                                                                                                                                                                                                                         4
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GWGQPHGG
                                                                                                                                                                                                                                                                                                                                                                                                                         GWGQPHGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              γď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; ilarity 100.0%; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunisation with metal-containing polypeptide
                                                                                                                                                                                                                                                       cattle; sheep; pig; bovine spongiform encephalopathy;
transmissable spongiform encephalopathy; TSE;
                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                             assay; scrapie
         971E-0000325.
971E-0000081.
971E-0000228.
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                                                        98WO-IE00007
                                                                                                                                                                                   Location/Qualifiers 28..61
                                                                                                                                               90..128
                                                                                                                                                          /note= "Synthetic sequence used against prpsc"
                                                                                                                                       /note=
                                                                                                                                                                                                                                                                                                                                                               peptide;
                                                                                                                         "Synthetic sequence against prpSC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scheller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                            prion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 55;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.094;
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                                                                                                                                                                                                                                             prpsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                       raise antibody
                                                                                                                                                                         raise antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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RESULT 12
AAB07316
В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention claims to provide a method for detecting transmissable spongiform encephalopathies (TSE) in animals and in animal carcasses. The method comprises of an immunological assay whereby the animal test sample is reacted with a labelled antibody against scrapie prion protein (prpSC) and the amount of bound labelled antibody is then detected. The anti-prpSC antibodies used in the assay are raised against fragments of the present synthetic peptide shown. The peptide fragments preferred by the inventors are shown in the features table. The method is claimed to be useful when applied to samples, particularly a cross-section of the spinal cord, from cattle, sheep and pig carcasses for detection of bovine spongiform encephalopathy (BSE) or scrapie.
                                               (WALL-)
(BBSR-)
WPI; 2000-387880/33
                       Норе Ј,
                                                                                      17-NOV-1998;
                                                                                                               27-OCT-1999;
                                                                                                                                        25-MAY-2000.
                                                                                                                                                                WO200029850-A1
                                                                                                                                                                                                                 Disulfide-bond Modified-site
                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                Key
                                                                                                                                                                                                                                                                                                       Mus sp
                                                                                                                                                                                                                                                                                                                                 bovine
                                                                                                                                                                                                                                                                                                                                             Mouse;
                                                                                                                                                                                                                                                                                                                                                                     Mouse prion protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                17-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                        AAB07316;
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB07316 standard; protein; 208 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detecting pathogenic prion(s) in specific labelled antibody, used bovine spongiform encephalopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-447377/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O'Connor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ENFE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GWGQPHGG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GWGQPHGG 84
                                                                                                                                                                                                                                                                                                                               prion protein; spongiform ence
                                                              WALLAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
8; Conserv
                                                 BBSRC OFFICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENFER TECHNOLOGY LTD.
                       Barnard GJR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; ilarity 100.0%; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23; 25pp; English.
                                                            20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                      98FI-0002481
                                                                                                             99WO-FI00897
                                                                                                                                                                                                                          /note= "Repeat region consisting of tundem repeats of repeat unit: PHGGGWGQ (AAB07319)"
                                                                                                                                                                                                                                                                   Location/Qualifiers 37..68
                                                                                                                                                                                         membrane
                                                                                                                                                                                        /note= "C-terminal phospho-inositol glycolipid
membrane anchor (-GPI)"
                                                                                                                                                                                                                                                                                                                               ein; transmissible spongiform encephalopathy;
encephalopathy; BSE diagnosis; TSE; PrP.
                       Birkett CR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 55; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               animal carcasses - by reaction with to detect those carrying agents for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and scrapie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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RESULT 13
AAB07318
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is the mouse prion protein (PrP) sequence. Conversion of the normal cellular form of PrP into an aggregated, incomplete isoform is implicated in the pathogenesis of Transmissible spongiform Encephalopathies (TSEs). Examples of TSEs include Bovine spongiform Encephalopathy (BSE), scrapic, Creutzfeldt-Jakob disease (CJD) and Gerstmann-Straussler-Sheinker syndrome (GSS). The concentration of this protein in body fluid or tissue samples may be measured by an assay of the present invention, in which a presence of PrP indicates TSE. PrP antibody, which is then detected. The presence of PrP indicates TSE. PrP epitopes (AABO7320-B07326) are derived from the protease resistant core
                                                                                                  Норе Ј,
                                                                                                                                                                                                                                                                                                          Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                           Human; prion protein; bovine spongiform ence
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human prion protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB07318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB07318 standard; protein; 208 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                          WPI; 2000-387880/33.
                                                                                                                             (BBSR-)
                                                                                                                                                                 17-NOV-1998;
                                                                                                                                                                                         27-OCT-1999;
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                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of PrP that is occluded when the PrP is in an aggregated state.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel immunoassay for prion protein, used for the determination transmissible spongiform encephalopathies in bovines \,\cdot\,
                                                                                                                                       (WALL-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 GWGQPHGG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GWGQPHGG
                                                                                                                                        WALLAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
8; Conserv
                                                                                                                            BBSRC OFFICE.
                                                                                                 Barnard GJR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   208 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 41-42; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                        9
                                                                                                                                                                 98FI-0002481
                                                                                                                                                                                           99WO-FI00897
                                                                                                                                                                                                                                                                                                      /note= "Repeat region consisting of tandem repeats
of repeat unit: PHGGGWGQ (AABO7319)"
157...192
                                                                                                                                                                                                                                                                    /note= "C-terminal phospho-inositol glycolipid
membrane anchor (-GPI)"
                                                                                                                                                                                                                                                                                               208
                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers 29..69
                                                                                                                                                                                                                                                                                                                                                                                                              ein; transmissible spongiform encephalopathy;
encephalopathy; BSE diagnosis; TSE; PrP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                  Birkett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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Pred. No. 0.43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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Disclosure;

Page 43-44; 50pp; English

Novel immunoassay for prion protein, used transmissible spongiform encephalopathies

for the determination in bovines -

of.

Novel immunoassay for

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RESULT 14
AAB07327
           Query Match
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The present sequence is the mouse prion protein (PrP) sequence. Conversion of the normal cellular form of PrP into an aggregated, insoluble isoform is implicated in the pathogenesis of Transmissible spongiform Encephalopathies (TSEs). Examples of TSEs include Bovine spongiform Encephalopathy (BSE), scrapie, Creutzfeldt-Jakob disease
                                                                                                                                New immunoassay for prion protein, used for determination transmissible spongiform encephalopathies in mammals, compspecific capture antibody \, \cdot \,
                                                                                                                                                                                                                                                            (WALL-)
                                                                                                      Disclosure;
                                                                                                                                                                                                 WPI; 2000-399778/34
                                                                                                                                                                                                                              Hope J,
                                                                                                                                                                                                                                                                                                         17-NOV-1998;
                                                                                                                                                                                                                                                                                                                                        27-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse; prion protein; transmissible spongiform encephalopathy; bovine spongiform encephalopathy; TSE diagnosis; PrP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse prion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-OCT-2000
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                                                                                                   Page 41-42; 50pp; English.
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of repeat unit: PHGGGWGQ (AAB07319)"
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membrane anchor (-GPI)"
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          The present sequence is the human prion protein (PrP) sequence. Conversion of the normal cellular form of PrP into an aggregated, insoluble isoform is implicated in the pathogenesis of Transmissible spongiform Encephalopathies (TSEs). Examples of TSEs include Bovine Spongiform Encephalopathy (BSE), scrapie, Creutzfeldt-Jakob disease (CJD) and Gerstmann-Straussler-Sheinker syndrome (GSS). The concentration of this protein in body fluid or tissue samples may be measured by an assay of the present invention, in which a PrP epitope is captured by an antibody, which is then detected. The presence of PrP indicates TSE. PrP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CJD) and Gerstmann-Straussler-Sheinker syndrome (GSS). The concentra of this protein in body fluid or tissue samples may be measured by an assay of the present invention, in which a PrP epittope is captured by antibody, which is then detected. The presence of PrP indicates TSE. epitopes (AAB07320-B07326) are derived from the protease resistant oc of PrP that is occluded when the PrP is in an aggregated state.
                                                                                                                                                                                  New immunoassay for prion protein, used for c
transmissible spongiform encephalopathies in
specific capture antibody -
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                                                                                                                                                       Disclosure; Page 43-44; 50pp; English.
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bovine spongiform encephalopathy; TSE diagnosis; PrP.
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(AAB07320-B07326) are derived
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membrane anchor (-GPI)"
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of repeat unit: PHGGGWGQ (AAB07319)"
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CC of PFF that is occluded when the PFP is in an aggregated State.

XX Sequence 208 AA;

Overy Match 100.04; Score 55; DB 21; Length 208;

METCHES 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GNOPHOG 8

Db 34 GNOPHOG 41

Job time : 36.4545 accs 3. 2003, 15:28:34
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prion-related prot

major prion protei

major prion protei
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RESULT 2 S71041 major pric C;Species; C;Date: 27 C;Accessic R;Schatzl, submitted A;Referenc A;Molecule A;Referenc A;Cross-re R;Crhatzl J,Mol. Bil A;Title: F A;Referenc	RESULT 1 A53892 prion-related C;Species: Rat C;Date: 07-Oct C;Accession: A R;Liao, Y.C.; Lab. Invest. 5 A;Title: Cloni A;Reference nu A;Accession: A A;Status: prel A;Molecule typ A;Residues: 1- A;Cross-refere C;Superfamily: Query Match Best Local S Matches Qy 1 GWGQ		33 33 33 33 33 33 33 33 33 33 33 33 34 34
ion protein - black-handed spider s: Ateles geoffroyi (black handed 27-oct-1996 #sequence_revision 07-ion: S71041; S53630  1, H.M. d to the EMBL Data Library, April nce number: S71041 le type: DNA es: 1-232 <sch> references: EMBL:008309; NID:94743</sch>	protein - rat (fragment) tus norvegicus (Norway rat) -1994 #sequence_revision 07- 53892 Tokes, Z.; Lim, E.; Lackey, 7, 370-374, 1987 ng of rat "prion related pro mber: A53892; MUID:88037055; S3892 iminary e: mRNA 226 <lia> 226 <lia> 226 <lia> 210.0%; Score 5 imilarity 100.0%; Pred. N ; Conservative 0; Misma PHGG 8          </lia></lia></lia>	ALIGNMENTS	55 100.0 254 2 A23544 55 100.0 256 2 JU0268 55 100.0 256 2 S37149 55 100.0 256 2 A24281 55 100.0 257 2 A23545 55 100.0 257 2 JQ1900 55 100.0 260 2 S3629 55 100.0 264 2 S37137 55 100.0 264 2 A54330 41 74.5 395 2 T08350 41 74.5 521 2 E64862 40 72.7 1161 2 T45294 39 70.9 69 2 B89016 39 70.9 120 2 F866824
<pre>monkey (fragment) spider monkey) spider monkey 1997 #text_change 13-Aug-1999 1994 1994 276; PIDN:AAC50097.1; PID:g474377 .; Cohen, F.E.; Prusiner, S.B. ng primates. ; PMID:7837269 11poprotein; prion; scrapie; transmembrane</pre>	Oct-1994 #text_change 13-Aug-1999 A.; Woo, C.H.; Button, J.D.; Clawson, G.A.  PMID:2889848  PMID:2889848  1; PIDN:AAA41947.1; PID:g206392 10. 0.069; 10. 0.069; 11ches 0; Indels 0; Gaps 0;	NTS	major prion protei major prion protei prion protein - go major prion protei prion protei - gr major prion protei prion protei prion protei pentaxin PTX3 prec hypothetical prote probable membrane probable prephenat hypothetical prote protein B0213.5 [i hypothetical prote

Query Match

100.0%;

Score 55; DB 2;

Length 232;

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A;Molecule type: DNA
A;Residues: 1-203, 'R', 205-240 <SCW>
A;Cross-references: EMBL:U08303
C;Superfamily: major prion protein
C;Keywords: amyloid; brain; 9lycoprotein; lipoprotein; prion; scrapie;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-202, E', 204-239 <SCW>
A;Residues: 1-202, E', 204-239 <SCW>
A;Cross-references: EMBL:U08293; NID:g474344; PIDN:AAC50082.1; PID:g474345
C;Superfamily: major prion protein
C;Keywords: amyloid; brain; glycoprotein; lipoprotein; prion; scrapie; trai
                    ş
                                                                                                                                                                                                                                    R:Schaetzl, H.M.; da Costa, M.; Taylor, L.
J. MOL. Biol. 245, 362-374, 1995
A;Title: Prion protein gene variation among
A;Reference number: $53614; MUID:95139066;
A;Accession: $53621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     major prion protein - mandrill (fragment)
C:Species: Papio sphinx, Mandrillus sphinx (mandrill)
C:Date: 27-Oct-1996 #sequence_revision 14-Feb-1997 #text_change 13-Aug-1999
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C;Date: 28-Oct-1996  #sequence_revision 07-Feb-1997  #text_change 13-Aug-1999
C;Accession: S5363; S71042
R;Schaetzl, H.M.; da Costa, M.; Taylor, L.; Cohen, F.E.; Prusiner, S.B.
J. Mol. Biol. 245, 362-374, 1995
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A; Residues: 1-241 <SCH>
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hitted to the EMBL Data
A; Reference number: S71041
A; Accession: S71056
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                                                                                                                                                                                                                   A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:U08303; NID:g474364; PIDN:AAC50091.1; PID:g474365
R;Schaetzl, H.M.; da Costa, M.; Taylor, L.; Cohen, F.E.; Prusiner, S.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A; Accession: $71042
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submitted to the EMBL Data
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esidues: 1-239 <SCH>
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8; Conserv
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                                                                      100.0%; Score 55; DB 2; 100.0%; Pred. No. 0.073;
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Pred. No.
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                                                         Mismatches
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A;Molecule type: DNA
A;Residues: 1-10,'V',12-202,'E',204-245 <SCW>
A;Cross-references: EMBL:U08291: NID:g474340; PIDN:AAC50080.1; PID:g474341
C;Superfamily: major prion protein
C;Keywords: amyloid; brain; glycoprotein; lipoprotein; prion; scrapie; tran
                                                                                                                                                                                                                                                                                    R;Schatzl, H.M.
submitted to the EMBL Data
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A;Cross-references: EMBL:U08312
C;Superfamily: major prion protein
C;Keywords: amyloid; brain; glycoprotein; lipoprotein; prion; scrapie; transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 major prion protein - green monkey
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Date: 28-Oct.1996 #sequence_revision 07-Feb-1997 #text_change 13-Aug-1999
C;Accession: S53627; S71043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Prion protein gene variation among primates. A;Reference number: S53614; MUID:95139066; PMID:7837269 A;Accession: S53632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        major prion protein - Callicebus moloch (fragment)
C;Species: Callicebus moloch
C;Date: 27-Oct-1996 #sequence_revision 07-Feb-1997 #text_change 13-Aug-1999
                                                                                                                                                                                                                                                                          A; Reference number: A; Accession: S71043
                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-245 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: A; Accession: S53627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Title: Prion protein gene A; Reference number: S53614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Schaetzl, H.M.; da Costa, M.; Taylor, L.; Cohen, F.E.;
J. Mol. Biol. 245, 362-374, 1995
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J. Mol. Biol. 245, 362-374, 199
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A; Residues: 1-241 <SCH>
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8; Conserv
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                                                                                  Conservative
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63
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                                                                                                  100.0%; Score 55; 100.0%; Pred. No.
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                                                                                                    0.074;
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major prion protein - common marmoset (;Species: Callithrix jacchus (common marmoset) C;Species: Callithrix jacchus (common marmoset) C;Date: 28-Oct-1996 #sequence_revision 07-Feb-1997 #text_change 13-Aug-1999 C;Accession: S53634; S71047 R;Schaetzl, H.M.; da Costa, M.; Taylor, L.; Cohen, F.E.; Prusiner, S.B. J. Mol. Biol. 245, 362-374, 1995
                 A; Molecule type: DNA
A; Residues: 1-252 <SC
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A;Title: Infectious amyloid precursor gene sequences in primates used for experimental preference number: 136907; MUID:9508361; PMID:7991600
A;Accession: I61848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            major prion protein precursor - common squirrel monkey
C;Species: Saimiri sciureus (common squirrel monkey)
C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 13-Aug-1999
C;Accession: I61848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     major prion protein - Cercopithecus dianae
C;Species: Cercopithecus dianae
C;Species: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 13-Aug-1999
                                                          A; Status: nucleic acid sequence not shown
                                                                                A; Reference number: S53614; A; Accession: S53634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A:Residues: 8-10,'L',12-202,'R',204-239
:ss-references: EMBL:U08292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:U08292;
R;Schaetzl, H.M.; da Costa, M.; J
J. Mol. Biol. 245, 362-374, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-245 <SCH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: S;
R; Schatzl, H.M.
                                                                                                                       A; Title: Prion protein gene variation among
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Residues: 1-252 <RES>;Cross-references: EMBL:U15165; NID:g595852; PIDN:AAA68636.1; PID:g595853;
Perfamily: major prion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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8; Conserv
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EMBL: U08304
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                                                                                                       MUID:95139066;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 55; DB 2; Pred. No. 0.076;
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Pred. No. 0.074;
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                                                                                                       PMID: 7837269
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R;Loftus, B; Rogers, M. Gene 184, 215-219, 1997
A;Title: Characterization of a prion protein (PrP) gene A;Reference number: JC6175; MUID:97183665; PMID:9031631 A;Accession: JC6175.
A; Gene: PrP
C; Superfamily: major prion protein
C; Keywords: disulfide bond; prion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule typė: DNA
A; Residues: 1-209, 'E', 211-252 <SCW>
A; Cross-references: EMBL: U08295; NI
C; Superfamily: major prion protein
C; Keywords: amyloid; brain; glycopr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Schatzl, H.M. submitted to the EMBL Data Library,
                                                                          A;MoLecule type: DNA
A;Residues: 1-252 <LOP>
A;Cross-references: GB:U28334; NID:gl490412; PIDN:AAC48697.1;
C;Comment: This protein is a cellular protein, it is involved
                                                                                                                                                                                                                                                          C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 11-Apr-1997 #sequence_revision 09-May-1997
C;Accession: JC6175
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C;Date: 28-Oct_1996 #sequence_revision 07-Feb-1997 #text_change
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                                                               C; Genetics:
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J. Mol. Biol. 245, 362-374,
A:Title: Prion protein gene
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A; Residues: 1-209, 'E', 211-252 <SCW>
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Matches 8; Conser
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ilarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glycoprotein; lipoprotein; prion;
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Pred. No. 0.076;
Mismatches
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Pred. No. 0.076;
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                                                                                PID:gl490413
in the neuro
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R;Brown, P.; Goldfarb, L.G.; McComble, W.R.;
Neurology 42, 422-427, 1992
A;Title: Atypical Creutzfeldt-Jakob disease
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A;Residues: 8-240 <RE3>
A;Residues: 8-240 <RE3>
A;Cross-references: GB:M81930; NID:g190519; PIDN:AAB59443.1; PID:g190520
A;Cross-references: L.G.; McCombie, W.R.; Nieto, A.; Squillacote, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 8-117,119-253 <LIA>
A;Cross-references: GB:D00015; NID:g220015; PIDN:BAA00011.1; PID:g220016; GB:M13667; NID
A;Cross-references: GB:D00015; NID:g220015; PIDN:BAA00011.1; PID:g220016; GB:M13667; NID
B:TMaliavini, F.; Prelli, F.; Ghiso, J.; Bugiani, O.; Serban, D.; Prusiner, S.B.; Farlow
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A;Note: the deletion may be a polymorphism; the alternative deletion of 82-89
R;Liao, Y.C.J.; Lebo, R.V.; Clawson, G.A.; Smuckler, E.A.
Science 233, 364-367, 1986
A; Reference number: I58135;
A; Accession: I58135
                                                                                                                                                                                                                                                                                                                                                                                                                              A:Molecule type: DNA
A;Residues: 9-83,92-240 <RES>
A;Cross-references: GB:M81929; NID:g190517;
A;Accession: I68597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Deletion in the prion protein gene in a demented A;Reference number: I54322; MUID:93250789; PMID:1363802 A;Accession: I54322
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A:Residues: 58-72, 'X', 74-7
edrich, J.F.; Knopman,
Mol. Genet. 1, 443-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Amyloid protein of Gerstmann-Straeussler-Scheinker disease (Indiana kindred) A;Reference number: S14078; MUID:91160504; PMID:1672107 A;Accession: S14078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Genomic structure of the human prion protein gene A;Reference number: A40372; MUID:91328137; PMID:1678248 A;Accession: A40372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Molecular cloning of a human prion protein cDNA. Reference number: A24173; MUID:86300093; PMID:3755672 cession: A24173
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C:Species: Homo sapiens (man)
C:Date: 25-Oct-1987 #sequence_revision 12-Apr-1996 #text_change 16-Jun-2000
C:Accession: A24173; A40372; A05017; S14078; I54322; I68597; I58135; I59184; I79633; I79
R:Kretzschmar, H.A.; Stowring, L.E.; Westaway, D.; Stubblebine, W.H.; Prusiner, S.B.; De
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N;Alternate names: 11K amyloid protein; 27-30K sialoglycoprotein; PrP 27-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B
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                                                                                                                                          A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-80,89-253 <PUC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Puckett, C.; Concannon, P.; C
Am. J. Hum. Genet. 49, 320-329,
                                                                                                                  A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A: Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: A05017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: A05017; MUID: 86261778; PMID: 3014653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:M13899; NID:g190467; PIDN:AAA60182.1; PID:g190468 R;Puckett, C.; Concannon, P.; Casey, C.; Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Status: not compared with conceptual translation
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lecule type: mRNA
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8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'X',74-76,'XX',79,'XXX',83-86;111-128,'V',130-150
Knopman, D.S.; List, J.F.; Olson, K.; Frey, W.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    æ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                     PMID: 1736177
                                                                                                                                                                                                                                  in an American
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIDN: AAB59442.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                patient
                                                                                                                                                                                                                                  family with an insert mutation
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                                G.D.; Wills,
                                                                                                                                                                                                                                                                                       Sheremata, W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PrP
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                                P.R.
                                                                                                                                                                                         major prion protein precursor - chimpanzee

C:Species: Pan troglodytes (chimpanzee)

C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 13-Aug-1999

C:Accession: I61847; S71060; S53615
                                                       A; Reference number: I36907; A; Accession: I61847
                                                                                                                  A; Title:
                                                                                                                                       R;Cervenakova, L.; Brown, P.; Goldfarb, L.G.; Nagle, Proc. Natl. Acad. Sci. U.S.A. 91, 12159-12162, 1994
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     A; Molecule
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                                                                                                               Infectious amyloid
                             translated
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DNA

from

GB/EMBL/DDBJ

precursor gene sequences in MUID:95083661; PMID:7991600

J.;

Pettrone,

70

primates used

for experimenta

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A;Introns: #status absent
A;Note: one intron occurs before the initiator codon
A;Note: one intron occurs before the initiator codon
A;Note: this gene is associated with Creutzfeld-Jakob disease (CJD), Gerstmann-Straus
C;Superfamily: major prion protein
C;Keywords: amyloid; blocked carboxyl end; brain; glycoprotein; lipoprotein; phosphat
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-230/Product: major prion protein #status predicted <MAT>
F;54-92/Region: 8-residue repeats (P-H-G-G-W-G-O)
                                                                                                                                                                                                                                                                      A;Title: Infectious amyloid precursor gene sequences in A;Reference number: I36907; MUID:95083661; PMID:7991600 A;Accession: I37032
                                                                                                                                                     A;Cross-references: EMBL:U15166; NID:g563208; PIDN:AAA68633.1; C;Superfamily: major prion protein
                                                                                                                                                                                                A;Status: preliminary; translated from A;Molecule type: DNA A;Residues: 1-253 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                         major prion protein precursor - gorilla
C;Species: Gorilla gorilla (gorilla)
C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 13-Aug-1999
C;Accession: I37032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;231-253/Domain: carboxyl-terminal propeptide #status predicted <CF;179-214/Disulfide bonds: #status predicted F;179-214/Disulfide site: carbohydrate (Aso) (covalent) #status predi F;181,197/Binding site: carbohydrate (Aso) (covalent) #status predi F;230/Modified site: GPI-anchor ethanolamine amidated carboxyl end
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A;Map position: 20pter-20p12
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A; Residues: 60-67 <GOL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;112-134/Domain: transmembrane #status predicted <TM1>
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                                                                                                                                                                                                                                                                                                                                                      enakova, L.; Brown, P.; Goldfarb, L.G.; Nagle, J.; Natl. Acad. Sci. U.S.A. 91, 12159-12162, 1994
                                                                          Local
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nes 8; Conserv
1 GWGQPHGG
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8; Conser
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                                                                                                                                             prion protein
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Pred. No.
                                             Score 55; DB 2; Pred. No. 0.076; Mismatches
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                                                                                             Length 253;
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A;Molecule type: DNA
A;Residues: 1-210,'R',212-253 <SCH>
A;Cross-references: EMBL:U08296
C;Superfamily: major prion protein
C;Superfamily: major prion; glycoprotein; lipoprotein; prion; scrapie; transmembrane pro
Search completed: January 3, 2003, 15:33:13 Job time: 13.2727 secs
                                                                                                            В
                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:U08308; NID:g474374; PIDN:AAC50096.1; PID:g474375 A;Note: the source was designated as Symphalangus syndactylus A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1994 ("Operfamily: major prion protein")
                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-253 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Title: Prion protein gene variation among primates. A; Reference number: S53614; MUID:95139066; PMID:7837269 A; Accession: S53635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prion protein - siamang
C;Species: Hylobates syndactylus (siamang)
C;Date: 15-Jul-1995 #sequence_revision 19-Apr-1996 #text_change 13-Aug-1999
C;Accession: S53635
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A;Residues: 1-23 <SGW>
A;Residues: 1-25 <SGW>
A;Coss-references: EMBL.U08296; NID:g474350; PIDN:AAC50085.1; PID:g474351
A;Cross-references: EMBL.U08296; NID:g474350; DID:g474351
A;Chaetzl, H.M.; da Costa, M.; Taylor, L.; Cohen, F.E.; Prusiner, S.B.
J. Mol. Biol. 245, 362-374, 1995
A;Title: Prion protein gene variation among primates.
A;Reference number: S53614; MUID:95139066; PMID:7837269
A;Accession: S53615
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R:Schhatzl, H.M.

R:Schhatzl, H.M.

A:Reference number: S71041

A:Accession: S71060
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Matches 8; Conserv
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                                                                                                      1 GWGQPHGG 8
||||||||
56 GWGQPHGG 63
                                                                                                                                                                                                           Local Similarity
nes 8; Conserv
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                                                                                                                                                                                                             Score 55; DB 2; Length 253; Pred. No. 0.076; ; Mismatches 0; Indels
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Result
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-i- FUNCTION: THE FUNCTION OF PRP IS NOT KNOWN. PRP IS ENCODED IN THE
-HOST GENOME AND IS EXPRESSED BOTH IN NORWAL AND INFECTED CELLS.
-i- SUBUNIT: PRP HAS A TENDENCY TO AGGREGATE YIELDING POLYMERS CALLED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cercopithecinae;
NCBI_TaxID=9565;
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Eukaryota; Metazoa; Chordata; Craniata; Ve
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Cercopithecinae; Theropithecus.
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MAJOR PRION PROTEIN.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
4 X 8 AA TANDEM REPEATS OF P-H-G-G-G-G.
Q.
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2.
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                                                                                                                       GPI-anchor;
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                                                                                               BY SIMILARITY
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Pred. No.
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                                                                                                                                                                                                                                          (See http://www.isb-sib.ch/announce/
                                                                                                                       Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.041;
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                                    (POTENTIAL).
OF P-H-G-G-G-W-G-
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Best Local S
Matches 8
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01-FEB-1995
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Major prion
                                                             CARBOHYD
CARBOHYD
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REPEAT
                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed.
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SEQUENCE
                                                                                         CHAIN
                                                                                                                                                  InterPro; IPR000817; Prion.
Pfam; PF00377; prion; 1.
SMART; SM00157; PRP; 1.
                                                                                                                                                                               EMBL; U08293; AAC50082.1; -. HSSP; P04925; 1AG2.
                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
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REPEAT
                                                                                                           Prion; Brain;
NON_TER
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                                                    DOMAIN
                                                                                DISULFID
                                                                                                   SIGNAL
                                                                                                                              PROSITE; PS00291; PRION_1; 1. PROSITE; PS00706; PRION_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aotus trivirgatus (Night monkey) (Douroucouli).
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                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95139066; PubMed=7837269;
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49
                                                                                                                                                                                                                                               European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor DISEASE: PRP IS FOUND IN HIGH QUANTITY IN THE BRAIN OF HUWANS ANIMALS INFECTED WITH THE DECEMERATIVE NEUROLOGICAL DISEASES KICKEUTZFELDT-JAKOB DISEASE (CJD), GERSTMANN-STRAUSSLER SYNDROME
                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE PRION FAMILY
                                                                                                                                                                                                                                                                                               (GSS), SCRAPIE, BOVINE SPONGIFORM ENCEPHALOPATHY (BSE), TRANSMISSIBLE MINK ENCEPHALOPATHY (TME), ETC.
                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GWGQPHGG
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                                                                                                             Glycoprotein;
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26104 .
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BY SIMILARITY.

MAJOR PRION PROTEIN.

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

5 X 8 AA TANDEM REPEATS OF P-H-G-G-G-G.

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2.
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4.
                                                                                                                     GPI-anchor;
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Pred. No.
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                                                                                                                                                                                                                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                      There are no rest
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                                                                                                                   Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                    Prusiner S.B.;
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Aotinae; Aotu
                                                  (POTENTIAL).
OF P-H-G-G-G-W-G
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Best Local
                                                                                                                                                        DISULFID CARBOHYD
                                                                                                                                                                                                                    NON_TER
      REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Prion protein gene variation among primates.";
J. Mol. Biol. 245:362-374(1995).
-i- FUNCTION: THE FUNCTION OF PRP IS NOT KNOWN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U08312; AAC50100.1; HSSP; P04925; 1AG2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre European Bioinformatics Institute. There are no restricted the succession of the succession
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                                                                                                                                     CARBOHYD
                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                             PROSITE; PS00
Prion; Brain;
                                                                                                                                                                                                                                                                               PROSITE; PS00291; PRION_1; 1. PROSITE; PS00706; PRION_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIO_CALMO P40248;
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                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000817; Prion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schatzl H.M., Dacosta M., Taylor L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95139066; PubMed=7837269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9523;
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(Rel. 31, Last sequence update)
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239

    Last annotation update)
    precursor (PrP) (PrP27-30) (PrP33-35C) (Fragment).

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BOVINE SPONGIFORM ENCEPHALOPATHY (BSE),
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BY SIMILARITY.
MAJOR PRION PROTEIN.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
5 X 8 AA TANDEM REPEATS OF P-H-G-G-G-Q.
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                                                                                                                                                                                                                                                           Repeat;
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                                                                                                                                                                                                                                                           Signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           collaboration
L outstation -
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Query Match
Best Local Similarity
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01-FEB-1995
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REPEAT
                                                                                                                       DISULFID CARBOHYD
                                                                                                                                                                                                                                                              SMART; SM00157; rar,
PROSITE; PS00291; PRION_1; 1.
PROSITE; PS00706; PRION_2; 1.
PROSITE; PS00706; PRION_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-95139066; PubMed-7837269;
Schatzl H.M., Dacosta M., Taylor L., Cohen F. Schatzl H.M., Dacosta M., Dacosta M., Taylor L., Cohen F. Schatzl H.M., Dacosta M., 
                                                                                                                                                                                                           SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000817; Pric
Pfam; PF00377; prion; 1.
SMART; SM00157; PRP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Prion protein gene variation J. Mol. Biol. 245:362-374(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata
Mammalia; Eutheria; Primates
Cercopithecinae; Mandrillus.
                                       REPEAT
                                                                                                                                                                 LIPID
                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U08303; AAC50091.1; -. HSSP; P04925; 1AG2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                     CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor. DISEASE: PRP IS FOUND IN HIGH QUANTITY IN THE BRAIN OF HUMANS FAIMALS INFECTED WITH THE DEGENERATIVE REUROLOGICAL DISEASES KUCREUTZFELDT-JAKOB DISEASE (CJD), GERSTMANN-STRAUSSLER SYNDROME (GSS), SCRAPIE, BOVINE SPONGIFORM ENCEPHALOPATHY (BSE), TRANSMISSIBLE MINK ENCEPHALOPATHY (TME), ETC.

SIMILARITY: BELONGS TO THE PRION FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOI. B101. 245:362-374(1995).

FUNCTION: THE FUNCTION OF PRP IS NOT KNOWN. PRP IS ENCODED IN THE HOST GENOME AND IS EXPRESSED BOTH IN NORMAL AND INFECTED CELLS.
SUBUNIT: PRP HAS A TENDENCY TO AGGREGATE YIELDING POLYMERS CALLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the Swiss Institute of Bioinformatics
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Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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(Rel. 31, Last sequence update)
(Rel. 34, Last annotation updat
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               BY SIMILARITY.

N-LINKED (GLCMAC...) (POTENTIAL).

N-LINKED (GLCMAC...) (POTENTIAL).

5 X 8 AA TANDEM REPEATS OF P-H-G-G-G-G.

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Best Local :
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16-OCT-2001
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SEQUENCE
           DISULFID CARBOHYD
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                                                                       SIGNAL
                                                                                                                        InterPro; IPR000817; Prion. Pfam; PF00377; Prion; 1. PRION. PRION. SMART; SM00157; PRP; 1.
                                                                                                                                                                                        EMBL; U08291; AAC50080.1; -.
                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                       J. MOl. Biol. 245:362-374(1995).

-I- FUNCTION: THE FUNCTION OF PRP IS NOT KNOWN. PRP IS HOST GENOME AND IS EXPRESSED BOTH IN NORMAL AND IN-
-I- SUBUNIT: PRP HAS A TENDENCY TO AGGREGATE YIELDING "RODS".
                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Prion protein gene variation J. Mol. Biol. 245:362-374(1999)
                                                                                                 PROSITE; PS00291; PRION_1; PROSITE; PS00706; PRION_2;
                                                                                                                                                                           EMBL; U08292; AAC50081.1; HSSP; P04925; 1AG2.
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MEDLINE=95139066; PubMed=7837269;
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Mammalia; Eutheria;
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                                                  PROPEP
                                                             CHAIN
                                                                                      Prion;
                                                                                                                                                                                                                              or send an
                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                           between
                                                                                                                                                                                                                                                                                                        This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schatzl H.M., Dacosta M., Taylor L.,
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                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor DISEASE: PRP IS FOUND IN HIGH QUANTITY IN THE BRAIN OF HUMANS / ANIMALS INFECTED WITH THE DEGENERATIVE NEUROLOGICAL DISEASES KU CREUTZFELDT-JAKOB DISEASE (CJD), GERSTMANN-STRAUSSLER SYNDROME
                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE PRION FAMILY.
                                                                                                                                                                                                                                                                                                                                         (GSS), SCRAPIE, BOVINE SPONGIFORM ENCEPHALOPATHY (BSE), TRANSMISSIBLE MINK ENCEPHALOPATHY (TME), ETC.
                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboratic een the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                      Brain;
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8; Conserv
                                                                                                                                                                                                                            email to license@isb-sib.ch).
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(Rel. 31, Last sequence update)
(Rel. 40, Last annotation update)
protein precursor (PrP) (PrP27-30)
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                                                                                      GPI-anchor;
BY SIMILARITY.
N-LINKED (GLCN
N-LINKED (GLCN
                                                            3PI-anchor; Repeat; Signal.
BY SIMILARITY.
MAJOR PRION PROTEIN.
                                    REMOVED IN MATURE FORM (BY GPI-ANCHOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 55; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lor L., Cohen F.E.,
among primates.";
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(GLCNAC...
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SMART; SM00157; PRP; 1
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EMBL; U75387; AAB5
HSSP; P04925; 1AG2
                                                                                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                             the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cercopithecinae; Cercopithecus.
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Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                        SÜBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor. DISEASE: PRP IS FOUND IN HIGH QUANTITY IN THE BRAIN OF HUMANS A ANIMALS INFECTED WITH THE DEGENERATIVE MOLOGICAL DISEASES KU CREUTERELDT-JAKOB DISEASE (CJD), GERSTMANN-STRAUSSLER SYNDROME (GSS), SCRAPIE, BOVINE SPONGIFORM ENCEPHALOPATHY (BSE), TRANSMISSIBLE MINK ENCEPHALOPATHY (TME), ETC.
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                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE PRION FAMILY.
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AAB50626.1; -.
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EMBL/GenBank/DDBJ databases.
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Pred. No.
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(GLCNAC.
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Submitted (NOV-1996) to the EMBL/GGEBBANK/DDBJ databases.
Submitted (NOV-1996) to the EMBL/GGEBBANK/DDBJ databases.
FUNCTION: THE FUNCTION OF PRP IS NOT KNOWN. PRP IS ENCODED IN THE
HOST GENOME AND IS EXPRESSED BOTH IN NORMAL AND INFECTED CELLS.
                                                                                                                                   Pfam; PF00377; prion; () SMART; SM00157; PRP; 1
                                                                                                                                                                                                            modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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01-NOV-1997
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Q95174;
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                                                                                                                                                                   EMBL; U75388;
HSSP; P04925;
                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                         (GSS), SCRAPIE, BOVINE SPONGIFORM ENCEPHALOPATHY (BSE), TRANSMISSIBLE MINK ENCEPHALOPATHY (TME), ETC. SIMILARITY: BELONGS TO THE PRION FAMILY.
                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor. DISEASE: PRP IS FOUND IN HIGH QUANTITY IN THE BRAIN OF HUMANS A ANIMALS INFECTED MITH THE DECEMBRAIVE NEUROLOGICAL DISEASES KU CREUTZFELDT-JAKOB DISEASE (CJD), GERSTMANN-STRAUSSLER SYNDROME
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OF P-H-G-G-G-W-G-
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SMART; SM00157; PRP; 1.

PROSITE; PS00291; PRION_1; 1.

PROSITE; PS00706; PRION_2; 1.
                                                                                                                                                                  EMBL; U75385;
HSSP; P04925;
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Submitted (NOV-1996) to the EM
-!- FUNCTION: THE FUNCTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                      Cercopithecinae; Cercocebus.
NCBI_TaxID=9531;
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Mammalia; Eutheria; Primates;
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                                                                                                                                                        InterPro; IPR000817; Prion.
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                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor. DISEASE: PRP IS FOUND IN HIGH QUANTITY IN THE BRAIN OF HUMANS AND ANIMALS INFECTED WITH THE DEGENERATIVE MEMOLOGICAL DISEASES KURU, CREUTZPELDT-JAKOB DISEASE (CJD), GERSTWANN-STRAUSSLER SYNDROME (GSS), SCRAPIE, BOVINE SPONGIFORM ENCEPHALOPATHY (BSE), TRANSISSIBLE MINK ENCEPHALOPATHY (TME), ETC.
                                                                                                                                                                                                                                                                                                                                                              mitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
FUNCTION: THE FUNCTION OF PRP IS NOT KNOWN. PRP IS ENCODED IN THE HOST GENOME AND IS EXPRESSED BOTH IN NORMAL AND INFECTED CELLS.
SUBUNIT: PRP HAS A TENDENCY TO AGGREGATE YIELDING POLYMERS CALLED
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8; Conser
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(Rel. 35, Last sequence update)
(Rel. 35, Last annotation update)
protein precursor (PrP) (PrP27-30) (PrP33-35C) (Fragment).
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                                                                                                      Glycoprotein;
                                                                                                                                                                             AAB50628.1; -.
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  REMOVED IN MATURE FORM (BY SIMILARITY)
GPIT-ANCHOR (BY SIMILARITY).
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
5 X 8 AA TANDEM REPEATS OF P-H-G-G-G-U.
                                                                                                                                                                                                                                                                                                                                                                                                        Goudsmit J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                       GPI-anchor; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0 4 0 0 4 D
                                                                                     BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 55; DB 1;
Pred. No. 0.042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D35D105BBEC53108 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                         PRION PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 246;
                                                                                                      Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
              P-H-G-G-G-W-G-
                                                               SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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RESULT 11
PRIO_ATEPA
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIO_ATEPA
P51446;
01-OCT-1996
01-OCT-1996
01-OCT-1996
 LIPID
DISULFID
CARBOHYD
                                                                                              Prion;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Infectious amyloid precursor gene sequences in primates used for experimental transmission of human spongiform encephalopathy."; Proc. Natl. Acad. Sci. U.S.A. 91:12159-12162(1994).
-i- FUNCTION: THE FUNCTION OF PRP IS NOT KNOWN. PRP IS ENCODED IN THE HOST GENOME AND IS EXPRESSED BOTH IN NORMAL AND INFECTED CELLS.
-i- SUBUNIT: PRP HAS A TENDENCY TO AGGREGATE YIELDING POLYMERS CALLED
                                                                                                                                                                       Pfam; PF00377; prion; 1 PRINTS; PR00341; PRION. SMART; SM00157; PRP; 1.
                                                                                                                                                                                                                            EMBL; U15164; AAA68634.1; -
HSSP; P04156; 1E1G.
InterPro; IPR000817; Prion.
                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Platyrrhini; Cebidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
REPEAT
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REPEAT
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                                                         PROPEP
                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cervenakova L., Brown P., Goldfarb L.G., Nagle J.,
Rubenstein R., Dubnick M., Glbbs C.J., Gajdusek D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRNP
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                                                                              CHAIN
                                                                                                                                    PROSITE;
                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-95083661; PubMed-7991600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor DISEASE: PRP IS FOUND IN HIGH QUANTITY IN THE BRAIN OF HUMANS / DISEASE: PRP IS FOUND THE DEGENERATIVE NEUROLOGICAL DISEASES K( ANIMALS INFECTED WITH THE DEGENERATIVE NEUROLOGICAL DISEASES (CENTZFELDT-JAKOB DISEASE (CJD), GERSTMANN-STRAUSSLER SYNDROME (GSS), SCRAPIE, BOVINE SPONGIFORM ENCEPHALOPATHY (BSE),
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE PRION FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMISSIBLE MINK ENCEPHALOPATHY (TME), ETC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GWGQPHGG
                                                                                                                  Brain;
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8; Conser
                                                                                                                                    PS00291; PRION_1; PS00706; PRION_2;
                                                                                                                                                                                                                                                                                                                                                                                                    the Swiss Institute of Bioinformatics and the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 34, Created)
(Rel. 34, Last sequence update)
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                                                                                                                Glycoprotein;
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                                                                                                              GPI-anchor;
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MAJOR PRION PROTEIN.
REMOVED IN MATURE FORM (BY SIMILARITY).
GPI-ANCHOR (BY SIMILARITY).
BY SIMILARITY
N-LINKED (GLCNAC. . ) (POTENTIAL).
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                                                                                              BY SIMILARITY
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                                                                                                                Repeat;
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                                                                                                                Signal
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Atelinae; Ateles.
                                                                                                                                                                                                                                                                                                                                                                              restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                      EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                      collaboration
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Best Local
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PRIO_CALJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P40247;
01-FEB-1995
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DISULFID
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REPEAT
                                      CHAIN
                                                   SIGNAL
                                                                Prion;
                                                                          PROSITE; PS00291; PRION_1; PROSITE; PS00706; PRION_2;
                                                                                                    SMART;
                                                                                                           Pfam; PF00377; prion; 1. PRINTS; PR00341; PRION.
                                                                                                                                               EMBL; U08304; AAC50092.1; HSSP; P04925; 1AG2.
                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                  modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                           use
                                                                                                                                                                                                                                    the European Bioinformatics Institute.
                                                                                                                                                                                                                                                   between
                                                                                                                                                                                                                                                                                                                                                                                                                           Schatzl H.M., Dacosta M., Taylor L., Cohen F.E., "Prion protein gene variation among primates."; J. Mol. Blol. 245:362-374(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE=95139066; PubMed=7837269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Callithrix jacchus (Common marmoset)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Major prion
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                                                                                                                                      InterPro; IPR000817; Prion
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(601. BLOI. 245:362-374(1995).

FUNCTION: THE FUNCTION OF PRP IS NOT KNOWN. PRP IS ENCODED IN THE FUNCTION OF PRP IS NOT KNOWN. PRP IS ENCODED IN THE HOST GENOME AND IS EXPRESSED BOTH IN NORMAL AND INFECTED CELLS.

HOST GENOME AND IS EXPRESSED BOTH IN NORMAL AND INFECTED CELLS.
                                                                                                                                                                                                                                                                                    (GSS), SCRAPIE, BOVINE SPONGIFORM ENCEPHALOPATHY (BSE), TRANSMISSIBLE MINK ENCEPHALOPATHY (TME), ETC. SIMILARITY: BELONGS TO THE PRION FAMILY.
                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor DISEASE: PRP IS FOUND IN HIGH QUANTITY IN THE BAAIN OF HUMANS AND ANIMALS INFECTED WITH THE DEGENERATIVE NEUROLOGICAL DISEASES KURD CREUTZFELDT-JAKOB DISEASE (CJD), GERSTMANN-STRAUSSLER SYNDROME
                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GWGQPHGG
                                                             Brain;
                                                                                                   SM00157; PRP; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
8; Conserv
                                                                                                                                                                                                                         non-profit
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230
229
178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
Glycoprotein;
1 22
23 229
230 252
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229 229
178 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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34,
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90

    Last sequence update)
    Last annotation update)
    precursor (PrP) (PrP27-30)

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66 2
74 3
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27718 MW;
                                                                                                                                                                                                license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata; Craniata; Vertebrata; Eutele
Primates; Platyrrhini; Callitrichidae;
                                                                                                                                                                                                                        rmatics Institute. There are no restrictions institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
GPI-anchor; Repeat; Signal.
BY SIMILARITY.
MAJOR PRION PROTEIN.
REMOVED IN MATURE FORM (BY SIMILARITY).
GPI-ANCHOR (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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5 X 8 AA TANDEM REPEATS OF P-H-G-G-W-G-
Q.
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SEQUENCE
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REPEAT
           PROPEP
LIPID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cebus apella (Brown-capped capuchin)
Eukaryota; Metazoa; Chordata; Crania
                                                                                             PRINTS; PR00341; PRION SMART; SM00157; PRP; 1.
                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=95139066; PubMed=7837269; Schatzl H.M., Dacosta M., Taylor L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Platyrrhini; Cebidae;
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                                                           Prion;
                                                                   PROSITE; PS00291; PRION_1; 1. PROSITE; PS00706; PRION_2; 1.
                                                                                                                  Pfam; PF00377; prion;
                                                                                                                                          EMBL; U08295; AAC50084.1; -. HSSP; P04156; 1E1G.
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                                                                                                                                                                                            entities
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                                                                                                                                                                                                                                                                                                                                                                                    "Prion protein gene variation among primates.";
J. Mol. Biol. 245:362-374(1995).
-i- FUNCTION: THE FUNCTION OF PRP IS NOT KNOWN. PRP
HOST GENOME AND IS EXPRESSED BOTH IN NORMAL AND
                                                                                                                                                                                                                                                                                                                                                                                                           J. Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                InterPro; IPR000817; Prion.
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                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor. DISEASE: PRP IS FOUND IN HIGH QUANTITY IN THE BRAIN OF HUMANS AND ANIMALS INFECTED WITH THE DECEMERATIVE NEUROLOGICAL DISEASES KURU. CREUTZFELDT-JAKOB DISEASE (CJD), GERSTMANN-STRAUSSLER SYNDROME
                                                                                                                                                                                                                                                                         (GSS), SCRAPIE, BOVINE SPONGIFORM ENCEPHALOPATHY TRANSMISSIBLE MINK ENCEPHALOPATHY (TME), ETC. SIMILARITY: BELONGS TO THE PRION FAMILY.
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8; Conser
                                                                                                                                                                             requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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252
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(Rel. 31, Last sequence update)
(Rel. 34, Last annotation update)
protein precursor (PrP) (PrP27-30)
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5 X 8 AA
BY SIMILARITY.

MAJOR PRION PROTEIN.

REMOVED IN MATURE FORM (BY SIMILARITY).

GPI-ANCHOR (BY SIMILARITY).

BY SIMILARITY.
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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Pred. No. 0.043;
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Q95211;
01-NOV-1997
CARBOHYD
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                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                            Species with apparent resistance to infection by prions.";
Gene 184:215-219(1997).
-I- FUNCTION: THE FUNCTION OF PRP IS NOT KNOWN. PRP IS ENCODED IN THE
HOST GENOME AND IS EXPRESSED BOTH IN NORMAL AND INFECTED CELLS.
-I- SUBBURIT: PRP HAS A TENDENCY TO AGGREGATE YIELDING POLYMERS CALLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Major prion protein precursor (PrP) (PrP27-30) PRNP OR PRP.
                         CHAIN
                                   SIGNAL
                                                  Prion; Brain;
                                                                PROSITE; PS00291; PRION_1; PROSITE; PS00706; PRION_2;
                                                                                            SMART;
                                                                                                       Pfam; PF00377; prion; 1. PRINTS; PR00341; PRION.
                                                                                                                                              EMBL; U28334; AAC48697.1; -. HSSP; P10279; 1DWY.
                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=New Zealand white; MEDLINE=97183665; PubMed=9031631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Characterization of a prion protein (PrP) gene from species with apparent resistance to infection by price
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Coftus B., Rogers M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                  DISEASE: PRP IS FOUND IN HIGH QUANTITY IN THE BRAIN OF HUMANS ANIMALS INFECTED WITH THE DEGENERATIVE NEUROLOGICAL DISEASES KI CREUTZFELDT-JAKOB DISEASE (CJD), GERSTMANN-STRAUSSLER SYNDROME (GSS), SCRAPIE, BOVINE SPONGIFORM ENCEPHALOPATHY (BSE), TRANSMISSIBLE MINK ENCEPHALODATHY (THERE)
                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE PRION FAMILY.
                                                                                                                                                                                                                                                                                                                TRANSMISSIBLE MINK ENCEPHALOPATHY (TME), ETC
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(Rel. 35, Last sequence up)
(Rel. 35, Last annotation
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llarity 100.0%;
Conservative (
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                                                GPI-anchor; Repeat; Signal
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N-LINKED (GLCNAC. . .) (POTENTIAL).
5 X 8 AA TANDEM REPEATS OF P-H-G-G-
          N-LINKED (GLCNAC. . .) (POTENTIAL)
                     MAJOR PRION PROTEIN.
                                     POTENTIAL.
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Pred. No. 0.043;
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01-FEB-1995
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 8-253 FROM N.A. der Kuyl A.C., Dekker J.T., Goudsmit J.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
FUNCTION: THE FUNCTION OF PRP IS NOT KNOWN. PRP IS ENCODED IN THE HOST GENOME AND IS EXPRESSED BOTH IN NORMAL AND INFECTED CELLS.
-!- SUBUNIT: PRP HAS A TENDENCY TO AGGREGATE YIELDING POLYMERS CALLED
                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schatzl H.M., Dacosta M., Taylor L., Cohen F.E. "Prion protein gene variation among primates."; J. Mol. Biol. 245:362-374(1995).
                       Pfam; PF00377; prion; PRINTS; PR00341; PRIO SMART; SM00157; PRP;
                                                                             EMBL; U08297; AAC50086.1; -. EMBL; U75389; AAB50624.1; -. HSSP; P04925; IAG2.
                                                                                                                                     entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Colobus guereza (Black-and-white colobus monkey)
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P40251;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95139066; PubMed=7837269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
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les .8; Conserv
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                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE PRION FAMILY.
                                                                                                                                                                                                                                                              (GSS), SCRAPIE, BOVINE SPONGIFORM ENCEPHALOPATHY (BSE), TRANSMISSIBLE MINK ENCEPHALOPATHY (TME), ETC.
                                                                IPR000817; Prion
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protein precursor (PrP) (PrP27-30)
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PROSITE;

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PRION\_1;

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KW Prion; Brain; Glycoprotein; GPI-anchor; Repeat; Signal.

FT SIGNAL

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Search completed: January 3, 2003, 15:29:18

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## ALIGNMENTS

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Q16409; Q16407;
Q1-NOV-1996 (Tri
01-NOV-1996 (Tri
01-JUN-2002 (Tri
Cochran E.J., Bennett D.A., Cervenakova L., Kenney K., Bernard B., Foster N.L., Benson D.F., Goldfarb L.G., Brown P.; "Familial Creutzfeldt-Jakob disease with a five-repeat octapeptide insert mutation."; Neurology 47:727-733(1996).
EMBL; S80539, AAB21334.1; -.
EMBL; S79978; AAB35416.1; -.
                                                                                                                                                                   SEQUENCE OF 1-89 FROM N.A.
MEDLINE-96057178; PubMed=7572084;
Oda T., Kitamoto T., Tateishi J., Mitsuhashi T.,
Oguni E., kato Y., Tominaga I., Yanai K.;
"Prion disease with 144 base pair insertion in a
line.";
                                                                                                                                                                                                                                                                                MEDLINE-92140671; PubMed=1736177;
Brown P., Goldfarb L. G., McCombie W.R., Nieto A., Squillacote D.
Sheremata W., Little B.W., Godec M.S., Gibbs C.J. Jr., Gajdusek
"Atypical Creutzfeldt-Jakob disease in an American family with a
insert mutation in the PRNP amyloid precursor gene.";
                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                       SEQUENCE OF 1-81 FROM N.A. MEDLINE=96390485; PubMed=8797471;
                                                                                                                                      Acta Neuropathol. [3]
                                                                                                                                                                                                                                                        Neurology 42:422-427(1992).
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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SEQUENCE
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J. Mol. Biol. 289:1163-1178(1999).
EMBL; AFI13944; AAD13922.1;
InterPro; IPR002395; Kininogen.
InterPro; IPR000817; Prion.
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-97317556; PubMed-9174569;
Schatzl H.M., Wopfner F., Gilch S., von Brunn
"Is codon 129 of prion protein polymorphic in
                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                Pfam; PF00377; prion; 1.
PRINTS; PR00334; KININOGEN.
PRINTS; PR00341; PRION.
SMART; SM00157; PRP; 1.
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Schwarz T.F., Werner T., Schatzl H.M.;
"Analysis of 27 mammalian and 9 avian PrPs reveals high conser-
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE=99303687; PubMed=10373359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Muntiacus muntjak (Muntjak).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
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RESULT 5 097905 ID .0979 AC 0979

.097905 097905;

PRELIMINARY;

PRT;

141

AA

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RESULT
Q9TU20
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В
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Matches 8
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Best Local (
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                                                                                                                                                                                                                                                                                                                   Q9TU20
Q9TU20;
01-MAY-2000
01-MAY-2000
01-DEC-2001
                                                                                NON_TER
NON_TER
SEQUENCE
                                                                                                                          Pfam; PF00377; prion; 1. PRINTS; PR00341; PRION. SMART; SM00157; PRP; 1.
                                                                                                                                                                             susceptible lemur monkey.";
Submitted (AUG-1999) to the
EMBL; AF177293; AAD54335.1;
                                                                                                                                                                                                            SEQUENCE FROM N.A.
Gilch S., Schatzl H.M.;
"Unusual prion protein octarepeat structure
                                                                                                                                                                                                                                                                                               PRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Expression of Prion Protein in Human Lenses.";
"Expression of Prion Protein in Human Lenses.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AF139166; AAD24491.1;
InterPro; IPR000817; Prion.
                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-STRAIN 13/N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prion protein (Fragment).
Cavia porcellus (Guinea pig).
Eukaryota, Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                               PROSITE; PS00291; PRION_1;
                                                                                                                                                                                                                                                                           Eukaryota;
                                                                                                                                                                                                                                                                                     Varecia variegata variegata.
                                                                                                                                                                                                                                                                                                          Prion protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00157; PRP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00377; prion; 1. PRINTS; PR00341; PRION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10141;
[1]
                                                                                                                                                          InterPro; IPR000817; Prion.
                                                                                                                                                                    HSSP; P04925; 1AG2
                                                                                                                                                                                                                                                      NCBI_TaxID=87289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00291; PRION_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                  4
                                                                                                                                                                                                                                                                                                                                                                                                                  54 GWGQPHGG
տ
                   1 GWGQPHGG 8
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GWGQPHGG
                                       Similarity
8; Conser
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8; Conserv
                                                                                 124
124
                                                                                                                                                                                                                                                                                                                   0 (TrEMBLrel. 13, 00 (TrEMBLrel. 13, 11) (TrEMBLrel. 19, 11)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 AA;
                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117
                                                                                                                                                                                                                                                                 Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=OCULAR LENS;
                                                                                 13436 MW;
                                                                                                                                                                                                                                                                            Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11818 MW;
                                                 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                        0
                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                        EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                         Created)
                                      Score 55; DB
Pred. No. 0.1
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 55;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                Strepsirhini;
                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                 CC2C8A5A855A7C94 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     863A02472404EA05 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                 0.1;
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                                                            DB
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                                                           6;
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                                                                                                                                                                                                                                                                 Lemuridae; Varecia.
                                                                                                                                                                                                                                                                                                                    update)
                                        0
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                                                                                                                                                                                                             the highly
                                                           Length 124;
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                                        Indels
                                        0
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                                       Gaps
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SQ PT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
  Query Match
Best Local S
Matches 8
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9MZ17;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER
                                                                                                                                      HSSP: P10279; 1DWY.
InterPro; IPRO08817; Prion.
Pfam; PF00377; Prion; 1.
PRINTS; PR00341; PRION.
SMART; SM00157; PRP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ovis aries (Sheep).
                                                                                                                                                                                                                                      susceptible sheep.";
Submitted (MAY-2000) to the
Submitted (MAY-2000) to the
EMBL; AF267507; AAF91403.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9MZ17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00377; prion; 1. PRINTS; PR00341; PRION. SMART; SM00157; PRP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wopfner F., Weidenhofer G., Schneider R., von Brunn A., Gilch S., Schwarz T.F., Werner T., Schatzl H.M.;
"Analysis of 27 mammalian and 9 avian PrPs reveals high conservation of flexible regions of the prion protein.";
of 10 protein protein.";
J. Mol. Biol. 289:1163-1178(1999).
                                                                                                 PROSITE; PS00291; PRION_1; 1.
                                                                                                                                                                                                                                                                                                                        Knowles D.P.;
                                                                                                                                                                                                                                                                                                                                           Herrmann
                                                                                                                                                                                                                                                                                                                                                                                                 Bovidae; Caprinae; Ovis.
NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prion protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P10279; 1DWY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF117311; AAD19982.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99303687; PubMed=10373359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-PBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tursiops
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tursiops truncatus (Atlantic bottle-nosed dolphin). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prion protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1999
01-JUN-2002
                                                                                                                                                                                                                                                                                                  "Detection of PrPc in peripheral blood mononuclear cells
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9739;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             σ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GWGQPHGG 8
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  Similarity
8; Conserv
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8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS00291; PRION_1;
                                                                                                                                                                                                                                                                                                                                         L.M., Davis W.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR000817; Prion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 10, Last sequence update) (TrEMBLrel. 21, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel.
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43
                                                                              AA;
                                                                                14428 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15066 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cetartiodactyla;
                  100.0%;
                                                                                                                                                                                                                                                          to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
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  0;
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                                                                                                                                                                                                                                                            EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                         Η.,
                  Score 55; DB 6
Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 55; DB 6
Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79BE306E2AAA187C CRC64;
                                                                              4E2D296C6C8022E2 CRC64
  Mismatches
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                                                                                                                                                                                                                                                                                                                                     Wardrop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cetacea; Odontoceti; Delphinidae;
                                     DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B
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  0;
                                     Length 143;
                                                                                                                                                                                                                                                                                                                                       M.-S.,
  Indels
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                                                                                                                                                                                                                                                                                                                                         Gambetti P.
                                                                                                                                                                                                                                                                                                  of scrapie
0;
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Gaps
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0;
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097911
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RESULT 8
097694
 Query Match
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                                                                                                                                                                                                                                                     097694
097694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             097911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wopfner F., Weidenhofer G., Schneider R., voschwarz T.F., Werner T., Schatzl H.M.; "Analysis of 27 mammalian and 9 avian prps of flexible regions of the prion protein."; J. Mol. Biol. 289:1163-1178(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1999 (TREMBLIEL 10, 01-MAY-1999 (TREMBLIEL 10, 01-JUN-2002 (TREMBLIEL 21,
                                      "Is codon 129 of prion protein polymorphic animals?";
                                                              SEQUENCE FROM N.A.
MEDLINE=97317556; PubMed=9174569;
Schatzl H.M., Wopfner F., Gilch S
                                                                                                                                                                                                             01-MAY-1999 (TTEMBLrel. 10, 01-MAY-1999 (TTEMBLrel. 10, 01-JUN-2002 (TTEMBLrel. 21,
                                                                                                                                Mammalia; Eutheria;
Cervidae; Cervinae;
                                                                                                                                                         Eukaryota;
                                                                                                                                                                       Cervus nippon dybowskii
                                                                                                                                                                                                Prion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00377; prion; 1.
PRINTS; PR00334; KININOGEN.
PRINTS; PR00341; PRION.
SMART; SM00157; PRP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002395; Kininogen.
InterPro; IPR000817; Prion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF117326; AAD19997.1; -. HSSP; P10279; 1DWY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=PBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bovidae; Caprinae; Budorcas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Budorcas taxicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prion protein
SEQUENCE FROM N.A
                          Lancet 349:1603-1604(1997).
                                                                                                                   NCBI_TaxID=88066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00291; PRION_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99303687; PubMed=10373359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=37181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59
                                                                                                                                                                                                                                                                                                                                    32 GWGQPHGG
                                                                                                                                                                                                                                                                                                                                                   1 GWGQPHGG
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                                                                                                                                                                                                                                                                                                                                                                                      Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                           181
181 AA;
                                                                                                                               Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Cetartiodactyla; Ruminantia; Peo
Cervinae; Cervus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Metazoa;
                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                  (Fragment).
                                                                                                                                                                                                                                                                                                                                    39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Fragment).
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; Chordata; Craniata; Vertebrata; Eutel
; Charatiodactyla; Ruminantia; Pecora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          181
                                                                                                                                                                                                                                                                                                                                                                                                                                           19253 MW;
                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                 Gilch S
                                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                    Score 55; DB 6
Pred. No. 0.15;
                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                           A9001D086442E92A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                               von Brunn
                                                                                                                                             Ruminantia; Pecora;
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                                                   'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  reveals
                                                    human
                                                               A., Jager G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                Length 181;
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                                                   beings
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                                                                                                                                              Cervoidea;
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Best Local S
Matches 8
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HSSP; P10279; IDMY.
InterPro; IPR002395; Kininogen.
InterPro; IPR002817; Prion.
Pfam; PF00377; prion; 1.
PRINTS; PR00334; KININOGEN.
PRINTS; PR00334; PRION.
PRINTS; PR00341; PRION.
SMART; SM00157; PRP; 1.
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InterPro; IPR000817; Prion.
Pfam; PF00377; Prion; 1.
PRINTS; PR00374; KININOGEN.
PRINTS; PR00341; PRION.
SMART; SM00157; PRP; 1.
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J. Mol. Biol. 289:1163-1178(1999).
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J. Mol. Biol. 289:1163-1178(1999).
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                                                                                                                                                                                                                                             NON_TER
                                                                                                                                                                                                                                                                  PROSITE; PS00291; PRION_1; 1. PROSITE; PS00706; PRION_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-PBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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EMBL; AF113941; AAD13289.1;
HSSP; P10279; 1DWY.
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5 GWGQPHGG 42
GWGQPHGG
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                                                                                           h 100.0%;
Similarity 100.0%;
8; Conservative 0
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8; Conserv
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185 AA;
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llarity 100.0%;
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30
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Pred. No. 0.16;
0; Mismatches
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Pred. No. 0.16;
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RESULT 10
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Best Local
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097912;
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097693;
                                                                                                           Schwarz T.F., Werner T., Schatzl H.M.;

**Rhalysis of 27 mammalian and 9 avian PrPs reveals high conservation of flexible regions of the prion protein.";

J. Mol. Biol. 289:1163-1178(1999).

EMBL; AFI17328; AAD19999.1; *.

HSSP; P10279; IDMY.
                                                                                                                                                                                                                                                                                                                                                                       Bison bonasus (European bison).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
Bovidae; Bovinae; Bison.
NCBI_TaxID=9902;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00377; prion; 1.
PRINTS; PR00341; PRION.
SMART; SM00157; PRP; 1.
PROSITE; PS00291; PRION_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; NCBI_TaxID=9612;
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                                         InterPro; IPR001610; PAC. InterPro; IPR000817; Prion.
                                                                                                                                                                                                                                                    MEDLINE-99303687; PubMed-10373359; Wopfner F., Weidenhofer G., Schneider R.,
                                                                                                                                                                                                                                                                                                          TISSUE=PBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prion protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00706; PRION_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Canis lupus (Gray wolf).
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PRINTS;
                   Pfam; PF00377; prion;
                                                                                          InterPro; IPR002395; Kininogen
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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PR00334;
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8; Conserv
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195 AA;
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.A; 21097 MW;
KININOGEN
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Pred. No. 0.16;
Mismatches
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Best Local :
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Best Local :
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Interpro; IPR002395; Kininogen.
Interpro; IPR000817; Prion.
Pfam; PF00377; Prion; 1.
PRINTS; PR00334; KININOGEN.
PRINTS; PR00341; PRION.
SMART; SM00157; PRP; 1.
PROSITE; PS00291; PRION_1; 1.
PROSITE; PS00706; PRION_2; 1.
                       097696 PRELIMINARY;
097696;
01-MAY-1999 (TrEMBLrel. 10, C
01-MAY-1999 (TrEMBLrel. 10, L
01-JUN-2002 (TrEMBLrel. 21, L
Prion protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00086; PAC; 1.
SMART; SM00157; PRP; 1.
PROSITE; PS00291; PRION_1; 1.
PROSITE; PS00706; PRION_2; 1.
NON_TER 1 1
NON_TER 200 200
SEQUENCE 200 AA; 21674 MW;
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SEQUENCE
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PROSITE;
NON_TER
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"Analysis of 27 mammalian and 9 avian PrPs reveals high conservation of flexible regions of the prion protein.";
of Months and 9 avian PrPs reveals high conservation of the prion protein.";
J. Mol. Biol. 289:1163-1178(1999).
EMBL; AFIJ7319, AAD19990.1;
EMBL; AFIJ7319, AAD19990.1;
HSSP: P10279; IDWY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Capra nubiana (Nubian ibex).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRP.
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01-MAY-1999 (TrEMBLrel 10,
01-JUN-2002 (TrEMBLrel 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99303687; PubMed=10373359;
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                                                                                                                                                                                                                                                                                                                     31 GWGQPHGG
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8; Conserv
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8; Conser
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202 AA;
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21949 MW;
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Pred. No. 0.17;
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1 GWGQPHGG
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Query Match
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"~+ches 8; Conserva
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Best Local Similarity
Matches 8; Conser
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O97629;
O1-MAY-1999 (TrEMBLrel. 10, C
O1-MAY-1999 (TrEMBLrel. 10, I
O1-JUN-2002 (TrEMBLrel. 21, I
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SEQUENCE
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NON_TER
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O'Rourke K.I., Miller M.W., Wild
O'rourke in free ranging and
                                                                                                                                                                                                                                                                          Submitted (SEP-1998) to the EMBL; AF091558; AAC69626.1; HSSP; P10279; 1DWY.
                                                                                                                                                                                                                                                                                                                            "PrP alleles in free virginianus).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                Odocoileus virginianus (white-tailed deer).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoide
Cervidae; Odocoileinae; Odocoileus.
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SMART; SM00157; PRP; 1.
PROSITE; PS00291; PRION_1;
PROSITE; PS00706; PRION_2;
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                                                                                                                                                                    Pfam; PF00377; prion; 1.
PRINTS; PR00334; KININOGEN.
PRINTS; PR00341; PRION.
SMART; SM00157; PRP; 1.
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Pfam; PF00377; prion; 1.
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                                                                                                                                    PS00291; PRION_1; 1. PS00706; PRION_2; 1.
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202 AA;
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204 AA;
                 Conservative
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22154 MW;
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21860 MW;
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Last annotation updat
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                Score 55; DB 6
Pred. No. 0.17;
Mismatches
                                                                                     CA8AE68F2B49C81E CRC64;
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                                              Length 204;
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                 Indels
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Search completed: January 3, 2003, 15:31:54
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O'ROURKE K.I., Miller M.W., Wild M.A., Williams E.S.;
O'Rourke K.I., Miller M.W., Wild M.A., Williams E.S.;
TISSUE-BRAIN;
O'Rourke K.I., Miller M.W., Wild M.A., Williams E.S.;
Tryliams E.S.;
The control of the control
                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 8; Conserv
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
Cervidae; Odocoileinae; Odocoileus.
NCBI_TaxID-9874;
                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER
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SEQUENCE
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O9TST8:
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Prion protein (Fragment).
                                                                                                                                         36 GWGQPHGG 43
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                                                                                                                                                                                                                                                                                                                                                                                                             204 AA;
                                                                                                                                                                                                                                                                    100.0%; Score 55; DB 6; Length 204; ilarity 100.0%; Pred. No. 0.17; Conservative 0; Mismatches 0; Indels
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22181 MW; CA962B93FA84D4D3 CRC64;
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Database
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
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1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
6: /cgn2_6/ptodata/1,
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Match
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19.615 Million cell updates/sec
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US-09-076-721-46
US-09-076-721-46
US-09-128-450-18
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US-08-660-626-8
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US-08-68-162A-2
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Patent No.
GENERAL IN
                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/244,701B FILING DATE: 02-JUN-1994 CLASSIFICATION: 436 ATTORNEY/AGENT INFORMATION: NAME: FAUNCAL, Allan A. REGISTRATION NUMBER: 30,256 REFERENCE/DOCKET NUMBER: 8080-007 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                            TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Fishleign, ROWLL APPLICANT: Robson, Barry
APPLICANT: Mee, Roger P.
TITLE OF INVENTION: Fragments of Prion Proteins
TITLE OF SEGUENCES: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                     FEATURE:
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LOCATION:
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OTHER INFORMATION: of Y and denotes
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ZIP: 10036
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STATE: New Yorl
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o. 5773572
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US-09-823-494-26
US-09-823-494-28
US-09-823-494-28
US-09-550-374-1
US-08-509-261A-4
US-08-509-261A-4
US-08-600-666-10
US-08-600-666-10
US-08-600-626-10
US-08-613-939A-4
US-08-868-162A-24
US-09-031-166A-24
US-09-031-165A-24
US-09-031-165A-24
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US-08-244-7018-24
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OTHER INFORMATION:
US-08-244-701B-27
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US-08-244-701B-27
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NAME: FADUCCI, Allan A.
REGISTRATION NUMBER: 30,256
REFERENCE/DOCKET NUMBER: 8080
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
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APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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OTHER INFORMATION:
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STATE: New Yor
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Mee, Roger P.
WENTION: Fragments of Prion Proteins
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                   100.0%; Score 55; DB 1; larity 100.0%; Pred. No. 0.017; Conservative 0; Mismatches
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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/note= "X may be absent or present independently
of Y and denotes one or more amino acid(s)"
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/note= "Y may be absent or present independently
of X and denotes one or more amino acid(s)"
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Pred. No. 0.(
0; Mismatches
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US-09-076-721-24
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Sequence 24, Application US/09076721 Patent No. 6379905
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Robson, i
APPLICANT: Mee, Roge
TITLE OF INVENTION:
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TELECOMMUNICATION INFORMATION:
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CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
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OTHER INFORMATION:
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TYPE: amino acid
STRANDEDNESS: Single
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ZIP: 10036
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STATE: New Yor
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1155 Avenue
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(212) 869-8864/9741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fishleigh, Robert V.
                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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                                                                                                                                                                                                                                                           100.0%;
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4 GWGCPHGG 11

4 GWGCPHGG 11

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2.244.701B-30

upence 30, Application US/08244701B

cant No. 577572

SNEWAL INFORMATICH, Framework of Prion Proteins

MPLICANN: Fishleigh, Robert V.

APPLICANN: Mee, Roger P.

APPLICAN: Mee, Roger P.

TITLE OF INVENTION: Fishleigh, Robert V.

APPLICAN: Mee, Roger P.

TITLE OF INVENTION: ABOUNDESS: 67

CORRESSED Pennie & Edmonds

STER: New York

CORPTRE: New York

CORPTRE: New York

COMPTRE: New York

COMPTRE: READERSES: PRODENS: NO. 2005

SOTTWARE: PROCECULAR PROPERTY OF THE P
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GENERAL INFORMATION:

APPLICANT:

Fishleigh, Robert V.

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RESULT 5
US-09-076-721-27
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                                                                                                                                                                                                   Sequence 27, Application US/09076721 Patent No. 6379905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
APPLICANT: Fishleigh, Rob
APPLICANT: Robson, Barry
APPLICANT: Mee, Roger P.
TITLE OF INVENTION: Fragm
NUMBER OF SEQUENCES: 67
                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/076,721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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4 GWGQPHGG 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION:
OTHER INFORMATION:
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REGISTRATION NUMBER: 30,256
REFERENCE/DOCKET NUMBER: 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Modified-site
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                                                                                                      Robson, Barry
                                                                                                                                  Fishleigh, Robert V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Robson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
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          Fragments of Prion Proteins 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= Y
/note= "Y may be
of X and denotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= x
/note= "X may be absent or present independently
of Y and denotes one or more amino acid(s)"
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Pred. No. 0.017;
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one or more amino acid(s)"
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RESULT 6
US-09-076-721-30
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                                                                                                                                                                      Sequence 30, Application US/09076721 Patent No. 6379905 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fanucci, Allan A.
REGISTRATION NUMBER: 30,256
REFERENCE/DOCKET NUMBER: 8080
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                   TITLE OF INVENTION: Fraq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/076,721
                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
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                                                                                            NUMBER OF SEQUENCES:
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                              STREET:
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OTHER INFORMATION: /note= "Y may be absent or present independently
OTHER INFORMATION: of X and denotes one or more amino acid(s)"
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OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION:
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CLASSIFICATION:
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 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
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                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                   4 GWGQPHGG
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                              New York
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New York
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                                             E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1155 Avenue of the Americas
                                                                                                                                                      Fishleigh, Robert V.
                                                                                                                                       Robson, Barry
                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             869-8864/9741
                                                                                            Fragments of Prion Proteins 67
                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 55; DB 4; 100.0%; Pred. No. 0.017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= X
/note= "X may be absent or present independently
of Y and denotes one or more amino acid(s)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US 08/244,701
                                                                                                                                                                                                                                                                                                                                               0; 'Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8080-007
                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 18;
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                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                              Gaps
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy

Floppy disk

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US-09-076-721-30
                                                                                                                                                                                                                                                                                                                                                  US-08-244-701B-46
                                                                                                                                                                                                                                                                                                                 Sequence 46, Application US/08244701B Patent No. 5773572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                          TITLE OF INVENTION: Fragments of Prion Proteins NUMBER OF SEQUENCES: 67
                                                                                                                                                                                                                                       APPLICANT: Fishleigh, Robert V.
APPLICANT: Robson, Barry
APPLICANT: Mee, Roger P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 80
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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LOCATION: 18
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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APPLICATION NUMBER:
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                                                                                                                STATE: New York
                                                                                    COUNTRY: UZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: /label= X
OTHER INFORMATION: /note= "X is absent or present independently of Y
OTHER INFORMATION: and denotes one or more amino acid(s)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212) /90 TELEFAX: (212) 869-8864/9741
                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Fanucci, Allan A. REGISTRATION NUMBER: 30,256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                      4 GWGQPHGG 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GWGQPHGG 8
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                                                                                                     U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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PatentIn Release #1.0, Version #1.25
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/note= "Y may be absent or present
of X and denotes one or more amino
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Best Local Similarity
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                                                      TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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LENGTH: 26 amino acids
TYPE: amino acid
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APPLICATION NUMBER: US,
FILING DATE: 02-JUN-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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MELEX: 66141 PENNIE
TO SEQ ID N
                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: CLASSIFICATION:
                                                                                                       TELEFAX:
                                                                                                                         TELEPHONE:
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                                                                                                                                                                                                                        FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
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TELEFAX: (212) 869-8864/9741
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             STRANDEDNESS:
                                             LENGTH:
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                           amino acid
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                                          26 amino acids
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Robson, Barry
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                                                                                                          (212) 869-8864/9741
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linear
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                                                                                                                         (212) 790-9090
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Pred. No. 0.024;
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US-09-823-494-18
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CURRENT FILING DATE: 1998-08-03
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN VEr. 2.0
SEQ ID NO 18
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Best Local Similarity
Matches 8; Conserv
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APPLICANT: Caughey, Byron W
APPLICANT: Chabry, Joelle
APPLICANT: Priola, Susette
TITLE OF INVENTION: Inhibitors of Formation of Protease Resistant Prion
FILE REFERENCE: 50121
CURRENT APPLICAMENT
                                                                                                                  SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 18
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APPLICANT: Priola, Susette
TITLE OF INVENTION: Inhibitors of Formation of Protease Resistant Prion
TITLE OF INVENTION: Protein
FILE REFERENCE: 50121
                                                                                                                                                 PRIOR APPLICATION NUMBER: 09/128,450
PRIOR FILING DATE: 1998-08-03
NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/823,494
CURRENT FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                                     APPLICANT: Chesebro, Bruce W
APPLICANT: Caughey, Byron W
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                                                                                                                                                                                                                                                                                                                                                                         equence 18, Appli
atent No. 6355610
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                                                             TYPE: PRT
ORGANISM: Hamster sp.
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TYPE: PRT
ORGANISM: Hamster sp
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RESULT 12
US-08-509-261A-2
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Best Local Similarity
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                                                                    Sequence 2, Application US/08509261A Patent No. 5763244
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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                            APPLICANT:
APPLICANT:
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APPLICANT:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/242,188
FILING DATE: 13-MAY-1994
CLASSIFICATION: 435
CLASSIFICATION: 435
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MEDIUM TYPE: Floppy disk
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TELECOMMUNICATION INFORMATION:
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NAME: Bosicevic, Karl
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
 TITLE OF INVENTION:
                                                                                                                                                                          56 GWGQPHGG
                                                                                                                                                                                                                                                                                                 ORGANISM: HUMAN PRION PROTEIN, HuPrP
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2200 Sand Hill Road
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                          Telling, Glenn
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                                        Prusiner, Stanley B. Scott, Michael R.
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                                                                                                                                                                                                                                                                                                                                                 linear
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                                                                                                                                                                                                                                                                                                                               peptide
                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                             100.0%;
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Method of Detecting Prions in a Sample and Transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28,807
                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                              Score 55; E
Pred. No. 0.
                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                            DB 1;
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  Animal Used fore
                                                                                                                                                                                                                                                          Length 253;
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NUMBER OF SEQUENCES: 4

ADDRESSEE: Bozicevic & Reed, LLP STREET: 285 Hamilton Avenue, Suite 200 CITY: Palo Alto STATE: CA

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Best Local Similarity
Thes 8; Conserve
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Sequence 8, Ap
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atent No. 5789655
GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: BOZICEVIC, Karl
REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 6510
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650.327-3400
                                                                                                                                                                                                                                                    TITLE OF INVENTION: TRA
TITLE OF INVENTION: EPI
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/
FILING DATE: 31-UU-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                 SOFTWARE: ASCIII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                           APPLICANT: Stanley B. Prusiner APPLICANT: Glenn C. Telling APPLICANT: Fred E. Cohen APPLICANT: Michael R. Scott
                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                       STREET: 2200 Sand Hill Road, Suite 100 CITY: Menlo Park
STATE: California
                 APPLICATION NUMBER: US/08/660,626 FILING DATE:
                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 GWGQPHGG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: sir
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: UZIP: 94301
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                                                                                                                                                       94025
                                                                                                                                                                                                                                                                                                                       Glenn C. Telling
Fred E. Cohen
Michael R. Scott
                                                                                                                                                                       USA
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IBM Compatible
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                                                                                                                                                                                                                                                                                         TRANSGENIC ANIMALS EXPRESSING EPITOPE-TAGGED PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 55; DB 1 100.0%; Pred. No. 0.22;
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US-08-692-892-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 579290
   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Prusiner, Stanley B.
APPLICANT: Scott, Michael R.
APPLICANT: Telling, Glenn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 854-0875 INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Valeta Gregg
REGISTRATION NUMBER: 35,127
REFERENCE/DOCKET NUMBER: 0753
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 322-5070
                                                           TOPOLOGY: linear MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION: NAME: Bozicevic, Karl
                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acid
                                                                                                                                                                                                 RECISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 322-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Karl Bozicevic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                              FILING DATE: 3
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Menlo Park
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nes 8; Conserv
                                                                                                         STRANDEDNESS:
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                                               ORGANISM:
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                                                                                                                                      253 amino acids
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linear
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                                               HUMAN PRION PROTEIN, HuPrP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide
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                                                                                                         single
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854-0875
NO: 2:
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   100.0%;
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   Score 55;
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Pred. No. 0.22;
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Length 253;
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-713-939A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08713939A

Patent No. 5846533

GENERAL INFORMATION:

APPLICANT: Prusiner, Stanley B.
APPLICANT: Williamson, R. Anthony
APPLICANT: Burton, Dennis R.

TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
NUMBER OF SEQUENCES: 86

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 2200 Sand Hill Road

CITY: Menlo Park

STATE: CA
Search completed: January 3, 2003, 15:34:26 Job time: 12 secs
                                                                              Db
                                                                                                                 οy
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US-08-713-939A-2
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                                                                                                                                                  Query Match
Best Local Similarity
Matches 8; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/713,939A
FILING DATE: 13-SEP-1996
CLASSIFICATION: 436
CRASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BOZICEVIC, Karl
REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 06510/059001
TELECOMMUNICATION INFORMATION:
TELECHONE: 415-854-9575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                          1 GWGQPHGG 8
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56 GWGQPHGG 63
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56 GWGQPHGG 63
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                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 415-854-0875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
                                                                                                                                                100.0%; Score 55; DB 2; Length 253; illarity 100.0%; Pred. No. 0.22; Conservative 0; Mismatcher
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Database
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Maximum DB seq
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
       Published_Applications_AA: *

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep: *

2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep: *

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep: *

4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep: *

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep: *

6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep: *

7: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep: *

9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep: *

9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep: *

10: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep: *

11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep: *

12: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep: *

13: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep: *

14: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep: *
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Gapop 10.0 ,
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Listing first 45 summaries
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                                                                                                                                     US-09-939-780-2
10 US-09-147-761-2
10 US-09-904-987-3
10 US-09-919-172-57
10 US-09-943-906-2
10 US-10-106-574-5
10 US-10-106-574-7
10 US-10-106-574-7
10 US-10-106-574-8
               US-10-109-551-2

US-10-109-551-4

US-10-109-551-8

US-10-109-551-8

US-10-109-551-10

US-09-943-906-3

US-10-115-984-2
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US-09-943-906-4
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(without alignments)
23.825 Million cell updates/sec
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 57, Appli
Sequence 2, Appli
Sequence 6, Appli
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45	44	43	42	41	40	39	38	37	36	35	34	$\frac{\omega}{\omega}$	32	31	30	29	28	27	26	25	24	23	22	21	20
36.5	37	37	37	37	37	37	3 8	3 8	38	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40.5
66.4	67.3	67.3	67.3	67.3	67.3	67.3	69.1	69.1	69.1	72.7	72.7	72.7	72.7	72.7	72.7	72.7	72.7	72.7	72.7	72.7	72.7	72.7	72.7	72.7	73.6
67	696	677	242	242	100	40	5179	5179	5179	1244	1244	1239	1239	1236	1236	1231	1231	1219	1219	1214	1214	774	774	44	387
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US-09-864-761-44423	US-09-925-300-1253	US-09-006-298-21	US-09-764-898-199	US-09-764-853-609	US-10-001-835-172	US-08-424-550B-552	US-09-833-263-1068	US-09-922-217-1068	US-10-025-380-1068	US-10-007-747-46	US-09-945-901-46	US-10-007-747-52	US-09-945-901-52	US-10-007-747-6	US-09-945-901-6	US-10-007-747-48	US-09-945-901-48	US-10-007-747-50	US-09-945-901-50	US-10-007-747-54	US-09-945-901-54	US-10-007-747-42	US-09-945-901-42	US-08-424-550B-519	US-09-866-987-9
Sequence 44423, A	Sequence 1253, Ap	Sequence 21, Appl		Sequence 609, App	Sequence 172, App	Sequence 552, App	Sequence 1068, Ap	Sequence 1068, Ap	Sequence 1068, Ap	Sequence 46, Appl	Sequence 46, Appl	Sequence 52, Appl	Sequence 52, Appl	6	Sequence 6, Appli	48	48	50,	50,	Sequence 54, Appl	54,	42,	Sequence 42, Appl	Sequence 519, App	Sequence 9, Appli

# ALIGNMENTS

RESULT 1 US-09-939-780-2

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; OTHER INFORMATION: Description of Artificial Sequence:prion protein ; OTHER INFORMATION: specific synthetic peptide US-09-939-780-2
                                                                                                         RESULT 2
US-09-147-761-2
                                                                                                                                                                                    В
                                                     Sequence 2, Application US/09147761 Patent No. US20010010918A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: O'CONDOT, Michael
TITLE OF INVENTION: Immunological Assay for Spongiform Encephalopathies
FILE REFERENCE: 50002US
                                                                                                                                                                                                                                                                       Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09939780 Patent No. US20020168689A1
                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 09/147,761
PRIOR FILING DATE: 1999-03-03
PRIOR APPLICATION NUMBER: PCT/IE98/00007
                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 43
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
APPLICANT:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                  15
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                                                                                                                                                                                                    1 GWGQPHGG 8
                                                                                                                                                                                GWGQPHGG 22
                                                                                                                                                                                                                                                   l Similarity
8; Conserv
                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                     100.0%;
   IMMUNOLOGICAL ASSAY FOR ENCEPHALOPATHIES
                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                   Score 55; DB Pred. No. 0.0; Mismatches
                                                                                                                                                                                                                                                                     ; DB 9;
. 0.044;
                      SPONGIFORM
                                                                                                                                                                                                                                                                                      Length 43;
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RESULT 4
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                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: No. US20020037908Alactyl, Inc.
APPLICANT: No. US20020037908Alactyl, Inc.
TITLE OF INVENTION: Methods and Compositions for Controlling Pathological and Prepath
TITLE OF INVENTION: Protein Assembly or Aggregation
FILE REFERENCE: 42108/26146
CURRENT APPLICATION NUMBER: US/09/904,987
CURRENT FILING DATE: 2001-07-12
NUMBER OF SEO ID NOS: 7
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09904987 Patent No. US20020037908A1
                                                                                                                                 Matches
                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                   ORGANISM: homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: NCBI ENTREZ / XM_009567
DATABASE ENTRY DATE: 2001-04-17
RELEVANT_RESIDUES: (1)..(253)
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TELEFAX: 353-1-6606920
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                     LENGTH: 253
TYPE: PRT
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TOPOLOGY: unknown
MOLECULE TYPE: Amino
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FRENCH PC COMPATION
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: 1
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CELL TYPE:
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nes 8; Conserv
                                                              56 GWGQPHGG 63
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                                                                                               1 GWGQPHGG 8
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Pred. No. 0.044;
                                                                                                                                                Score 55; DB 10; Length 253; Pred. No. 0.21;
                                                                                                                                 Mismatches
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                                                                                                                               Gaps
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GENERAL INFORMATION:
APPLICANT: Faris, Mary
APPLICANT: Turner, Christopher M.
APPLICANT: Turner, Christopher M.
FILE OF INVENTION: PROSTATE CANCER MARKERS
FILE REFERENCE: PA-0036 US
CURRENT APPLICATION UNMBER: US/09/919,172
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/222,469
PRIOR APPLICATION NUMBER: 60/222,469
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 102
SOCTWARE: PERL Program
SEQ ID NO 57
LENGTH: 253
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
US-09-943-906-2
Sequence 2, Application US/09943906
Patent No. US20020150571A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Incyte ID No. US20020119463A1 1256895CD1 US-09-919-172-57
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Best Local S
Matches 8
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                   TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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56 GWGQPHGG 63
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mes 8; Conser
                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-5277
TELEFAX: 415-854-0875
                                                                                                                                                                APPLICATION NUMBER: 09/550,374
FILING DATE: <Unknown>
FILING BATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BOZICEVIC, Karl
REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 06510,
                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARRE: PASTASEO Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/943,906
EILING DATE: 30-Aug-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 2200 Sand Hill Road
                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP NUMBER OF SEQUENCES: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Prusiner, Stanley B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Menlo Park
LENGTH: 253 amino acids
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Burton, Dennis R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 55; DB 10; Length 253; 100.0%; Pred. No. 0.21; tive 0; Mismatches 0; Indels
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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-943-906-2
RESULT 8
US-10-106-574-7
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                                                                                                                                                                        ; ORGANISM: Murinae US-10-106-574-6
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; ORGANISM: Murinae gen. sp.
US-10-106-574-5
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LENGTH: 254
                                                                                                                                          Query Match
                                                                                                                                                                                                                               SEQ ID NO 6
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Best Local :
                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10
CURRENT FILING DATE: 2002-03-26
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                               RENERAL INFORMATION:
APPLICANT: Harris, David A.
APPLICANT: Stewart, Richard S.
TITLE OF INVENTION: Compositions and Methods for
FILE REFERENCE: 09789280.0003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENERAL INFORMATION:
APPLICANT: Harris, David A.
APPLICANT: Stewart, Richard S.
TITLE OF INVENTION: Compositions and Methods
FILE REFERENCE: 09789280.0003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/106,574
CURRENT FILING DATE: 2002-03-26
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                  LENGTH: 254
TYPE: PRT
                                                        63
                                                                                                              Local Similarity les 8; Conserv
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                                                        GWGQPHGG 70
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100.0%; Pr
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Pred. No. 0.21;
                                                                                                                            Score 55; DB 9
Pred. No. 0.21;
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                                                                                                               Mismatches
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; TYPE: PRT
; ORGANISM: Murinae gen.
US-10-106-574-7
                                                                                                                                                                                                                                                                             RESULT 10
US-09-943-906-1
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NUMBER OF SEQ ID NOS: 8

SOFTWARE: PatentIn version 3.1

SEQ ID NO 7

LENGTH: 254
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SEQ ID NO 8
LENGTH: 254
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                                                                                                                                                                                                        Sequence 1, Application US/09943906
Patent No. US20020150571A1
GENERAL INFORMATION:
APPLICANT: Prusiner, Stanley B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/10106574 Patent No. US20020164335A1
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Matches 8; Conser
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Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/106,574
CURRENT FILING DATE: 2002-03-26
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Harris, David A.
APPLICANT: Stewart, Richard S.
TITLE OF INVENTION: Compositions and Methods
FILE REFERENCE: 09789280.0003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Stewart, Richard S. TITLE OF INVENTION: Compositions and Methods for the Study and Diagnosis of Prion FILE REFERENCE: 09789280.0003

CURRENT APPLICATION NUMBER: US/10/106,574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Harris, David A. APPLICANT: Stewart, Richar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 254
TYPE: PRT
ORGANISM: Murinae gen.
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                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 2200 Sand Hill Road
COMPUTER READABLE FORM:
                                                                                                                                    TITLE OF INVENTION: ANTIBODIES SPECIFIC NUMBER OF SEQUENCES: 86
            COUNTRY: U.S.A.
ZIP: 94025
                                                 CITY: Menlo Park
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Burton, Dennis R.
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Pred. No. 0.21;
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                                                                                                                                                        FOR NATIVE PrP
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MEDIUM TYPE: Diskette

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RESULT 11
US-09-943-906-4
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APPLICANT: Prusiner, Stanley
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Matches 8; Conserv
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FILING DATE: 30-Aug-2001
CLASSIFICATION: CURKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/550,374
APPLICATION NUMBER: 09/550,374
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: BOZICEVIC, Karl
REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 06510/05900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 GWGQPHGG 70
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ATTORNEY/AGENT INFORMATION:
NAME: BOZICEVIC, Karl
REGISTRATION NUMBER: 28,807
REPERENCE/DOCKET NUMBER: 06510/059001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-5277
                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/550,374
FILING DATE: <Unknown>
                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/943,906
FILING DATE: 30-Aug-2001
CLASSIFICATION: - Unknown>
                                                                                                                                                                                                                                                                                                                         ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 2200 Sand Hill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Williamson, R. Anthony
Burton, Dennis R.
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
NUMBER OF SEQUENCES: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-5277
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                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                          STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Menlo Park
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; ORGANISM: Ovis aries US-10-109-551-4
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US-10-109-551-2
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                                                      SEQ ID NO 4
LENGTH: 256
                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/10109551 Publication No. US20020194635A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: DUNNE, PATRICK W.
APPLICANT: PIEDRAHITA, JORG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 2
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Best Local Similarity
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                                                                                                                                                                     APPLICANT: PIEDRAHITA, JORGE
TITLE OF INVENTION: TRANSGEBIC ANIMALS RESISTANT TO TRANSMISSIBLE
TITLE OF INVENTION: SPONGIFORM ENCEPHALOPATHIES
FILE REFERENCE: TAMK: 207US
CURRENT APPLICATION NUMBER: US/10/109,551
CURRENT FILING DATE: 2002-03-28
CURRENT FILING DATE: 2002-03-28
                                                                                            SOFTWARE: PatentIn Ver. 2.1
                                                                                                                  NUMBER OF SEQ ID NOS: 10
                                                                                                                                  PRIOR APPLICATION NUMBER: 60/280,549 PRIOR FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                       APPLICANT: DUNNE, PATRICK W. APPLICANT: PIEDRAHITA, JORG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.1
                                      TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 GWGQPHGG 66
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les 8; Conserv
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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Pred No 0.21;
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Pred. No. 0.21;
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APPLICANT: DUNNE, PATRICK W.

APPLICANT: PIEDRAHITA, JORGE
TITLE OF INVENTION: TRANSGENIC ANIMALS RESISTANT TO TRANSMISSIBLE
TITLE OF INVENTION: SPONGIFORM ENCEPHALOPATHIES
FILE REFERENCE: TAMK: 207US
CURRENT APPLICATION NUMBER: US/10/109,551
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: 60/280,549
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 256
TYPE: PAT
ORGANISM: Odocoileus hemionus hemionus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: DUNNE, PATRICK W.
APPLICANT: DUNNE, PATRICK W.
APPLICANT: DIEDRAHITA, JORGE
TITLE OF INVENTION: TRANSGENIC ANIMALS RESISTANT TO TRANSMISSIBLE
TITLE OF INVENTION: SPONGIFORM ENCEPHALOPATHIES
FILE REFERENCE: TAMK:207US
CURRENT APPLICATION NUMBER: US/10/109,551
CURRENT APPLICATION NUMBER: 60/280,549
PRIOR APPLICATION NUMBER: 60/280,549
PRIOR FILING DATE: 2001-03-30
INUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 6
LENGTH: 256
TYPE: PRT
ORGANISM: Odocoileus virginianus
US-10-109-551-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
US-10-109-551-8
Sequence 8, Application US/10109551
Publication No. US20020194635A1
GENERAL INFORMATION:
Search completed: January Job time : 6.36364 secs
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US-10-109-551-6
                                                                                                                                                               Query Match
Best Local S:
Matches 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/10109551 Publication No. US20020194635A1 GENERAL INFORMATION:
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59 GWGQPHGG 66
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59 GWGQPHGG 66
                                                                                                                                                               / Match 100.0%; Score 55; DB 9; Length 256; Local Similarity 100.0%; Pred. No. 0.21; res 8; Conservative 0; Mismatches 0; Indels
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Copyright (c) 1993 - 2003 Compugen Ltd
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(without alignments)
30.067 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
_	34	100.0	6	23	AAU11826	Peptide ligand for
2	34	100.0	87	22	ABB40848	Peptide #8354 enco
ω	34	100.0	87	22	ABB25012	Protein #7011 enco
4	34	100.0	87	22	AAM61707	Human brain expres
Çī	34	100.0	87	22	AAM74503	Human bone marrow
6	34	100.0	87	22	AAM34616	Peptide #8653 enco
7	34	100.0	87	23	ABG44369	Human peptide enco
8	34	100.0	269	21	AAB26446	Drosophila melanog
9	34	100.0	269	22	ABB68723	Drosophila melanoq
10	34	100.0	453	21	AAB20922	Drosophila odorant

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	
31	ω	31	31	31	31	31	31	31	31	31	31	31	ω L	31	31	31	31	31	31	3 1	31	31	31	31	32	32	32	32	32	32	ω	ω ω	34	ω 4
	•			•	•				•		•	•	•		•			•	•	•	•	91.2	•	•			•				•	97.1	100.0	100.0
118	116	100	91	80	69	65	47	45	42	21	21	21	21	20	20	20	20	20	20	20	20	20	16	12	484	251	177	142	128	128	301	298	754	55 4
21	22	21	22	21	22	21	23	21	22	23	23	22	18	22	22	22	22	21	20	19	19	12	17	19	22	22	22	16	20	15	20	20	23	22
AAY52541	AAU44203	AAY64671	AAU14672	AAY52548	AAU21012	AAB24836	AAM47704	AAB03863	AAB71931	AAU75379	AAU75372	AAB86331	AAW12384	AAE01995	AAE04428	AAE08740	AAE11049	AAY52559	AAY17756	AAW68295	AAW69959	AAR10540	AAR84070	AAW60537	ABG05597	AAU33248	AAU15989	AAR81311	AAY28360	AAR53332	AAY24022	402	8	AAU14133
KappaLAMP-Th fusio	Propionibacterium	Human 5' EST relat	Novel bone marrow	Murine Ig-kappa si		Plant SDF encoded	Fragment of a reco	Active human neuro		immun	Mouse kappa immuno	Ig-kappa chain lea	ď	Immunoglobulin (Ig	Human immunoglobul	Ο.	Human Ig (immunogl	Consensus murine I	rget signal p		Ig kappa chain lea	Eukaryotic signal		peptide	l human		Human novel secret	Rat monoclonal ant	Antibody light cha	03 light chai	CMRF-35-H9	5-H9	cidally	Human novel protei

## ALIGNMENTS

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RESULT 1
AAU11826
                                                                                                                                                                                                                                        Prion protein; Prp; ligand; octapeptide motif; scrapie; prion-associated disease; Creutzfeldt-Jakob disease; Gerstmann-Straussler-Scheinker disease; fatal familial insomnia;
          WPI; 2002-061944/08
                                 Hammond DJ, Wiltshire VR,
                                                         (VITE-) VI
                                                                                 05-APR-2000; 2000US-0543188
                                                                                                          05-APR-2001; 2001WO-US11150
                                                                                                                                  18-OCT-2001.
                                                                                                                                                          WO200177687-A2
                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                        chronic wasting
                                                                                                                                                                                                                                                                                                                                             AAU11826;
                                                                                                                                                                                                                                                                                                                                                                    AAU11826 standard; peptide; 6 AA.
                                                                                                                                                                                                                  feline spongiform encephalopathy; bovine spongiform encephalopathy;
transmissible mink encephalopathy; exotic ungulate encephalopathy;
                                                                                                                                                                                                                                                                                           Peptide ligand for Prion protein, PrP, #1.
                                                                                                                                                                                                                                                                                                                  26-MAR-2002 (first entry)
                                                         TECHNOLOGIES INC
                                                                                                                                                                                                         disease
                                  Carbonell R,
                                  Shen H;
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RESULT 2
ABB40848
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Best Local Similarity
Matches 6; Conser
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measuring human gene expression in a sample derived
                       The invention relates to a single exon nucleic acid
                                                     Claim 27;
                                                                               analyzing
                                                                                Human genome-derived single exon nucleic analyzing gene expression in human fetal
                                                                                                                            WPI; 2001-483447/52.
                                                                                                                                                        Penn
                                                                                                                                                                                    (MOLE-)
                                                                                                                                                                                                                 04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                        WO200157277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; foetal liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide #8354 encoded by human foetal liver single exon probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB40848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a ligand of less than 6 kD that binds to a polypeptide containing the sequence GlyTyrGlyGlnProHisGlyGly (A) or an analogue that is the retro-inverso isomer of (A). The sequence A is an octapeptide motif from the prion protein (PrP). The ligands are identified by binding assays with the peptide (A) or peptides containing (A). The ligands are used for detecting prion proteins (or prions) in biological or environmental samples, e.g. for diagnosis, also for
                                                                                                                                                                                                                              21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                            03-AUG-2000;
                                                                                                                                                                                                                                                                       26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                     04-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB40848 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 16; Page 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New ligands for prion proteins, useful for detection or removal or prions and for treating prion-associated diseases, recognize a spec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LLIWIP 6
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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                                                     NO 33483;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              gene expression; single exon nucleic acid probe
                                                                                                                                                     Chen
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                                                 639pp + sequence listing; English.
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Pred. No. 7.8e+05;
                                                                                                                                                       Rank
                                                                                                                                                       DR
                                                                                acid probes
liver -
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          probe for
from human foetal
                                                                                              useful
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                                                                                                                                                                                                                                                                                                                                                                                      04 - FEB - 2000;
26 - MAY - 2000;
30 - JUN - 2000;
03 - AUG - 2000;
                     By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                     measuring human gene expression in a sample derived from human heart (see ABA21535-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                The present invention relates to single exon
                                                                                                                                                                                            Claim 15;
                                                                                                                                                                                                                                  Single
                                                                                                                                                                                                                                                                                                                                                              21-SEP-2000;
27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  congenital heart disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200157274-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cardiovascular disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; gene expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein #7011 encoded by probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB25012 standard;
                                                                                                                                                                                                                                                                                                                    (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
          ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 LLIWIP 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLIWIP
                                                                                                                                                                                                                                                                                         SG
                                                                                                                                                                                                                                  exon nucleic acid probes for analyzing gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity
6; Conser
                                                                                                                                                                                                                                                                                                                    MOLECULAR DYNAMICS INC
                                                                                                                                                                                            SEQ
                                                                                                                                                                                                                                                                                         Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53
                                                                                                                                                                                                                                                                                                                                                        2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001WO-US00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                               2000GB-0024263
                                                                                                                                                                                            ID No 26782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ΑĄ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100
                                                                                                                                                                                                                                                                                         Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               heart; microarray; vascular system;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .0%;
                                                                                                                                                                                         530pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                          Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for measuring heart cell gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                          English.
                                                                                                                                                                                                                                                                                          DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22;
                                                                                                                                                                nucleic acid probes for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                    in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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RESULT 5
AAM74503
                                             δÃ
                                                                                            SXCCCCCCCX8
                                                                                                                                                                                                      Query Match
Best Local Similarity
Thehes 6; Conserv
                               В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
                                                             Matches
                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                     03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                           04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
                                                                                                               probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of
                                                                                                                                                                                                                               Penn
                                                                                                                                                                                                                                                                                                                                                                                              Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                            Sequence
                                                                                                                                                                                                Single
                                                                                                                                                                                                              WPI; 2001-483446/52
                                                                                                                                                                                                                                                                                                                                                                                                                      Human brain expressed single
                                                                                                                                                                                                                                                                                                                                                                                                                                       05-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM61707 standard;
                                                                                                                                                                        Example 4; SEQ ID NO:
                                                                                                                                                                                                                                             (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                           09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                         WO200157275-A2
                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                         epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                          30-JAN-2001; 2001WO-US00667
                                                                                                           the probes of the invention.
                                                                                                                                                        The present invention provides a number of single exon nucleic acid
                               48 LLIWIP 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48 LLIWIP 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LLIWIP 6
                                             1 LLIWIP 6
                                                                                                                                                                                                                              SG,
                                                                                                                                                                                               exon nucleic acid probes
                                                            6;
                                                                                                                                                                                                                              Hanzel DK,
                                                                                            87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87
                                                              Conservative
                                                                                                                                                                                                                                                           2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234639.
2000US-0236359.
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                                                                                                                                                                                                                                                                                                           2000US-0180312.
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                                                                                            AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                       33812; 650pp + Sequence Listing;
                                                                                                                                                                                                                              Chen W,
                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                      exon probe encoded protein SEQ ID NO: 33812.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 34; DE Pred. No. 54;
                                                                    Score 34;
Pred. No.
                                                                                                                                                                                                                              Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
                                                            mismatches
                                                                                                                                                                                              for analyzing gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                            DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
                                                                            22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                            Length 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indel.s
                                                            Indels
                                                                                                                                                                       English
                                                            0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                               in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                               human
                                                            0;
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                                                                                                                 RESULT 6
AAM34616
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                                                                                                                                                                               Matches
      WO200157272-A2
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Query Match
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26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234587.
27-SEP-2000; 2000US-0236559.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                         genetic
                                                         Probe; microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probes which are derived from bone marrow. They can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-488900/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   microarray; cancer;
Homo sapiens
                                                                                            Peptide #8653 encoded by probe for measuring placental gene
                                                                                                                                       17-OCT-2001
                                                                                                                                                                                                                    AAM34616 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides a number of single exon nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               analyzing gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200157276-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; bone marrow expressed exon; gene expression analysis; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human bone marrow expressed probe encoded protein SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM74503 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MOLE-)
                                                                                                                                                                                                                                                                                                                1 LLIWIP 6
||||||
48 LLIWIP 53
                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity tes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genome-derived single exon nucleic acid probes useful for
                                         disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO: 34809; 658pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87 AA;
                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001WO-US00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                           human; placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in human bone marrow
                                                                                                                                                                                                                    87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87
                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genomic sequences expressed in the human to measure gene expression in bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rank
                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                      34;
                                                           antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                        DB
                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English.
                                                                                                                                                                                                                                                                                                                                                                                                                                        87;
                                                                                              expression
                                                                                                                                                                                                                                                                                                                                                                                                 0,
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                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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THE PRESENCE OF A CONTRACT OF 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                á
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Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-FEB-2000; 2000US-180312P-
26-MAY-2000; 2000US-207456P-
30-JUN-2000; 2000US-0608408-
03-AUG-2000; 2000US-0632366.
                                                                                                                                                                                                                                                                                                                                                                                                         chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-tick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary hastiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                           WO200186003-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG44369 standard; Peptide; 87
                                                                                                                                                      30-JAN-2001; 2001WO-US00665
                                                                                                                                                                                                                                                                                                                Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity les 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LLIWIP 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genome-derived single exon nucleic acid probes useful
                                                                                                                                                                                                                                                                                                                                                             membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                  ciliary dyskinesis; pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hanzel
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001WO-US00663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                encoded by genome-derived single exon probe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               No 34885; 654pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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Pred. No.
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AAB26446 ID AAB2

AAB26446 standard;

Protein;

269

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RESULT

X A X

AAB26446

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                                                                                                                                                                             Complements of the 1230 open reduling traines derived from the 12014 occurred to included are a microarray comprising the novel set of probes; the novel set of probes which hybridise at high stringency to a concleic acid expressed in the human lung; measuring gene expression in a cample derived from human lung; measuring gene expression in a collection of detectably labeled nucleic acids derived from human lung comprising (a) contacting the array with carray; identifying exons in a eukaryotic genome, comprising contacting the eukaryote; and (b) detecting specific hybridisation of detectably confided nucleic acids from eukaryote lung mana, to a single exon probe, control of the eukaryote; and (b) detecting specific hybridisation of detectably confided nucleic acids from eukaryote lung mana, to a single exon probe, control of a probe is included in the above mentioned microarray; assigning exons to a single exon probe, comprising (a) identifying exons from genomic sequence by the method comprising (a) identifying exons from genomic sequence by the method comprising the exons in the expression of each of the exons in several crisues and/or cell types using hybridisation to a single exon confidence to the exons should be assigned to a single exon probe indicates that the exons should be assigned to a single exon probe indicates that confidence in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene confidence in the specification, or encoded by the probes in man lung derived mana and for identifying exons in a gene, particularly cusing human lung derived mana and for the study of lung diseases conclumnary alternative pulmonary histographs. Lunghand of encoder's disease.

Confidence is a constant the specification, or encoded by the probes in the constant pulmonary disease.

Confidence is a constant pulmonary histographs. Sandorme, sancoldosis, pulmonary histographs. Sandorme, sancoldosis, pulmonary histographs. Sandorme, sancoldosis.
                                                                                    Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                               pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a peptide/protein encoded by a single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid probes for measuring gene expression in a sample
from human lung comprising single exon nucleic acid probes hav
12614 nucleic acid sequences mentioned in the specification, complements or the 12387 open reading frames derived from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-SEP-2000; 2000US-234687P
27-SEP-2000; 2000US-236359P
04-OCT-2000; 2000GB-0024263
                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a spatially-addressable set of single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spatially-addressable
48
                                       1 LLIWIP 6
LLIWIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27; SEQ ID No 34034; 634pp; English.
                                                                                    6; Conserv
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53
                                                                                      Conservative
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DR
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                                                                                                                                Length 87;
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of.

23-FEB-2001

(first entry)

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QΥ
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Best Local Similarity
Matches 6; Conserv
                                                                                        WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                               odorant receptor DORS9. The odorant genes and proteins, such as those provided by the invention, are useful as they aid in the study of the olfactory organ in mammals, as well as aiding the understanding of the link between odour recognition and behaviour in insects. They also enable the identification of compounds capable of activating and inhibiting the receptors, allow the control of pest populations via the use of alarm odour ligands and via the use of ligands which interfere with the
  23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                                27-SEP-2001
                                                                                                               Drosophila melanogaster
                                                                                                                                       pharmaceutical.
                                                                                                                                                    Drosophila;
                                                                                                                                                                            Drosophila melanogaster polypeptide SEQ'ID NO 32961.
                                                                                                                                                                                                                             ABB68723;
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 75; 176pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel nucleic acid encoding an insect odorant receptor, for identifying modulator compounds that are useful in controlling pest population - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vosshall LB
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                                      23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                    26-MAR-2002
                                                                                                                                                                                                                                                    ABB68723 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is the previously identified Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYCO ) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Odorant receptor; fruit fly; DOR59; odour recognition; pest control
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interaction between odorant ligands and receptors associated with
                                                                                                                                                                                                                                                                                                                 24 LLIWIP 29
                                                                                                                                                                                                                                                                                                                              1 LLIWIP 6
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DB; AAA94845.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 melanogaster odorant receptor DOR59
                                                                                                                                                                                                                                                                                                                                                                                                                   269
                                                                                                                                                   developmental biology;
                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COLUMBIA NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amrein
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                                                                                                                                                                                                                                                    Protein; 269
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                   cell
                                                                                                                                                  signalling; insecticide,
                                                                                                                                                                                                                                                                                                                                                                            DB 21;
1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                        Lengt:h 269;
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RESULT 10
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Best Local
                                                                                                                                                                                                                                                                             Odorant receptor; Drosophila; olfactory receptor; G protein-coupled receptor; GPCR superfamily; transgenic insect; insect behaviour modification; pest control; pollinator attraction; biosensor; odour detection; odour identification; apiculture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryottes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL101840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid genes from Drosophila and interactions -
                     New nucleic acid encoding a Drosophila olfactory receptor, useful identifying modulating agents -  \\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent
                                                              WPI; 2000-543246/49.
N-PSDB; AAA72257.
                                                                                                    Carlson JR,
                                                                                                                                                                              25-JAN-2000; 2000WO-US01823
                                                                                                                                                                                                                                  WO200043410-A2
                                                                                                                                                                                                                                                           Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                  Drosophila odorant receptor DOR 56E.1.
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                                                                                                                                                                                                                                                                                                                                                                                                                               AAB20922 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 32961; 21pp + Sequence Listing; English
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                                                                                                                            (UYYA ) UNIV YALE.
                                                                                                                                                       25-JAN-1999;
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                                                                                                  Kim J,
                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                       99US-0117132
                                                                                                                                                                                                                                                                                                     Drosophila; olfactory receptor;
coop superfamily; transgenic insect;
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100.0%; F
tive 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         detection reagent for detecting for elucidating cell signalling
                                                                                                    рJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                453
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Pred. No. 1.7e+02;
Mismatches 0;
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Claim 12; Page 175-177; 303pp; English

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RESULT 11
AAU14133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cc which modulate expression of these genes, and in methods to identify receptor binding partners. The Drosophila odorant receptor nucleic acids commany also be used to identify corresponding genes in other insects, cs such as those which damage crops or transmit disease. The odorant cc such as those which damage crops or transmit disease. The odorant cc activity, to identify binding partners, as antigens to raise antibodies, cc and in methods to modify insect behaviour. The proteins may be also be used in methods to modify insect behaviour. The proteins may be also complication of behaviour modification. Such methods may be used to study or modify insect behaviour in response to odorants such as pheromones. Modification of insect behaviour has a wide range of applications, such as in pest control (e.g., by disrupting the feeding or mating behaviours of pest species), or for enhancing plant contains the feeding pollination (by attracting pollinator species). Odorant receptor proteins and/or nucleotides may also be used to identify appetite suppressants, to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local
N-PSDB; AAS22438.
                                                                                                                                                                                                                                                                                                                        WO200155437-A2
                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                               antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic
thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic; anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human novel protein #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            trap odours of a specific type, as biosensors for the detection of explosives, drugs, perfumes or pollutants, and in apiculture to modify the behaviour of bees, for example, to increase the production of roya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequences AAB20901-B20949 represent Drosophila melanogaster odorant receptors. These proteins function as olfactory receptors, and are thought to be members of the G protein-coupled receptor (GPCR) superfamily, which is characterised by the presence of 7 (Transmembrane helices. Nucleic acids encoding the Drosophila odorant transmembrane helices. Nucleic acids encoding the Drosophila odorant
                                                                            Tang YT,
                                                                                                                                                                            25-JAN-2000; 2000US-0491404
                                                                                                                                                                                                                        25-JAN-2001; 2001WO-US02623
                                                                                                                                                                                                                                                                         02-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-OCT-2001
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                                                                                                                             (HYSE-)
                                                                                                                                                                                                                                                                                                                                                                                                                     tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             jelly.
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                                  2001-451939/48.
                                                                                                                                                                                                                                                                                                                                                                                                                   regeneration;
                                                                                                                             HYSEQ
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                                                                              Liu C,
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                                                                                                                               INC
                                                                                 Drmanac
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                                                                                                                                                                                                                                                                                                                                                                                                                     immune disorder
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         asthma; osteoporosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                     The polypeptides are used to identify compounds which bind to the polypeptides. Polypucleotides of the invention are used as probes and primers, for sequencing, for chromosome or gene mapping, in the production of recombinant proteins, and in generating anti-sense DNA or RNA and in gene therapy. Polypeptides of the invention can be used to target drugs to a tumour, in assays to determine biological activity, to raise antibodies/elicit an immune response, to determine quantitative protein levels, as tissue markers, and to isolate receptors or ligands. Polypeptides of the invention may also be useful in treating platelet disorders, stem cell disorders, regenerating bone, cartilage, tendon, ligament and/or nerve tissue, wound healing, treating burns, promoting the proliferation, differentiation and survival of stem cells, as a contraceptive, treating osteoporosis and osteoarthritis, anaemia, and the proliferation of the proliferation of stem cells, as a contraceptive, treating osteoporosis and osteoarthritis, anaemia, and the proliferation of the proliferation differentiation and survival of stem cells is a contraceptive, treating osteoporosis and osteoarthritis, anaemia, and the proliferation differentiation and osteoarthritis, anaemia, and the proliferation of the proliferation differentiation and osteoarthritis, anaemia, and the proliferation differentia
                                                                                                                                  Matches
                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                             fungal infection or from autoimmunity, cancer, allergy, asthma, graft-versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory diseases, nervous system disorders, and infec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to polynucleotides encoding novel human proteins or their active domains. The polypeptides, polynucleotides and antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein expression or activity. The polypeptides can be used
                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                 The present sequence represents a protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  molecular weight markers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nervous system disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated polypeptides useful for treating anti-inflammatory diseases,
138 LLIWIP 143
                                                               1 LLIWIP 6
                                                                                                                                  Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                stroke, immune deficiencies resulting
                                                                                                                                                                                                                                                                 554 AA;
                                                                                                                                  Conservative
                                                                                                                                                                  100
                                                                                                                                                           .0%; Score 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        894pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  food supplements, and in antibody production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and for regenerating bone and cartilage
                                                                                                                                  0;
                                                                                                                                  Mismatches
                                                                                                                                                                                                     DB 22;
                                                                                                                                                                  .5e+02;
                                                                                                                                                                                              Length 554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                from bacterial, viral
                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                    infection
                                                                                                                               0;
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ABB92828
                              Tietjen
                                                                                                                                                                                                                               Arabidopsis thaliana
                                                                                                                                                                                                                                                               Herbicidal;
                                                                                                                                                                                                                                                                                                                                31-MAY-2002
                                                                                                                                                                                                                                                                                                                                                               ABB92828;
                                                                                                                                                                                                                                                                                                                                                                                               ABB92828 standard; Protein; 754 AA
WPI; 2002-269010/31.
                                                               (FARB ) BAYER AG
                                                                                               28-AUG-2001; 2001WO-EP09892
                                                                                                                               28-AUG-2001; 2001WO-EP09892
                                                                                                                                                                                               WO200210210-A2
                                                                                                                                                                                                                                                                                            Herbicidally active polypeptide SEQ ID NO 2039.
                              ζ,
                              Weidler
                                                                                                                                                                                                                                                              plant;
                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                              agriculture;
                                                                                                                                                                                                                                                               herbicide
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AC XXX DT XXX DX

Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences

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RESULT 13
AAY24023
        THE COCCOCCA SERVING COCCOCCA SERVING COCCOCCA COCCOCCA COCCA COCC
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are
                        The present sequence represents a novel receptor, CMRF-35-H9, which binds immunoglobulin M (IgM). CMRF-35-H9, a CMRF-35-H9 extracellular domain peptide or a vector encoding these, can be used to modulate an immune response in a patient or to block or inhibit a humoral immune response in a patient. This is particularly useful in a patient who has or is about to receive a transplant. The CMRF-35-H9 receptor or extracellular
                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                        Human immunoglobulin M
                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-458446/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9936438-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY24023 standard;
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                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAX86359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OMOH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               promyelocytic leukemia; leukemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CMRF-35-H9 receptor; immunoglobulin M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human CMRF-35-H9 receptor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ORDE-) ORDER
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                                                                                                                                                                                                                                                                   immunomodulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       humoral immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity es 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LLIWIP 6
                                                                                                                                                                                                               ω,
                                                                                                                                                                                                               Page 33; 40pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         herbicides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
     to antibodies,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          response; transplant; myeloid leukemia,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SISTERS OF MERCY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein; 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2039;
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                                                                                                                                                                                                                                                                                        receptor CMRF-35-H9, useful for
                                                                                                                                                                                                               English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IN QUEENSLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IgM;
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) receptor
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transplant. A ligand/antigen construct that binds CMRF-35-H9 can be us to load a protective antigen or a stimulatory antigen into an antigen presenting cell. The level of CMRF-35-H9 in a patient sample can be determined to diagnose myeloid leukemia in a patient. An increased level of CMRF-35-H9 or decreased level of promyelocytic leukemia is diagnost of leukemia.
The present sequence represents a novel receptor, CMRR-35-H9, which binds immunoglobulin M (IgM). CMRR-35-H9, a CMRR-35-H9 extracellular domain peptide or a vector encoding these, can be used to modulate an immune response in a patient or to block or inhibit a humoral immune response in a patient. This is particularly useful in a patient who has or is about to receive a transplant. The CMRR-35-H9 receptor or extracellular domain binds to antibodies, which are then no longer free to bind to the
                                                                                             Claim 12;
                                                                                                                                                       N-PSDB; AAX86358
                                                                                                                                                                   WPI; 1999-458446/38
                                                                                                                                                                                           Hart DNJ
                                                                                                                                                                                                                                                               14-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      promyelocytic leukemia; leukemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human CMRF-35-H9 receptor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY24022;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
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                                                                                                                     immunomodulation
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                                                                                                                                 immunoglobulin
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                                                                                            Fig 2; 40pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             receptor;
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                                                                                                                                                                                                                 OF SISTERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 response;
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                                                                                                                                                                                                                                        98NZ-0329582
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                                                                                                                                                                                                                                                                                                                                               /note= "putative IgM binding domain" 178...201
                                                                                                                                                                                                                                                                                                                                                                                14..301
/label= mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                    /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                               /label= signal_peptide
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83.3%;
                                                                                                                                Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunoglobulin M; IgM; immunomodulation;
                                                                                             English
                                                                                                                              receptor CMRF-35-H9,
                                                                                                                                                                                                                                                                                                                                    "transmembrane region"
                                                                                                                                                                                                                                                                                                                                                                                                       "encoded by CTC
                                                                                                                                                                                                                 OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transplant;
                                                                                                                                                                                                                 MERCY IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301
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1; Mismatches
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. 2.8e+02;
tches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transplant. A ligand/antigen construct that binds CMRF-35-H9 can be used to load a protective antigen or a stimulatory antigen into an antigen presenting cell. The level of CMRF-35-H9 in a patient sample can be determined to diagnose myeloid leukemia in a patient. An increased level of CMRF-35-H9 or decreased level of promyelocytic leukemia is diagnostic of leukemia.
Chimeric human Ab expression vectors are constructed by inserting the Ab heavy and light chain variable region-encoding cDNA isolated from hybridomas producing a mouse or rat monoclonal Ab reacting with the ganglioside GM2 respectively into an expression vector for use in animal cells which contains the human Ab heavy a light chain constant region-encoding cDNA. The expression vectors
                                                                                                                     Disclosure;
                                                                                                                                                 Humanised antibody specific for ganglioside GM2 - used for producing a cytocidal effect on cancers such as melanoma, neuroblastoma and glioma.
                                                                                                                                                                                                                   WPI; 1994-126857/16.
N-PSDB; AAQ45430.
                                                                                                                                                                                                                                                                   Shitara K;
                                                                                                                                                                                                                                                                                                                                               07-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                             07-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                            17-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                            AU9346181-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Monoclonal antibody; Ab; ganglioside GM2; chimera; chimeric antibody; expression vector; heavy; light; chain; hypervariable region; CDR; constant region; hybridoma; Ig; immunoglobulin; KM-796; KM-750; KM-603; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR53332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR53332 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                  Hanai N,
                                                                                                                                                                                                                                                                                                              (KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rat rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KM-603 light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
nes 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 LLIWVP 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LLIWIP 6
                                                                                                                                                                                                                                                                                Hasegawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 AA;
                                                                                                                     Page 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first
                                                                                                                                                                                                                                                                                                                                                                             93AU-0046181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label - CDR1
70..76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= CDR2
                                                                                                                                                                                                                                                                                  Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97.1%;
83.3%;
                                                                                                                   191pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117
                                                                                                                                                                                                                                                                                  Koike
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 33; DB 20; Pred. No. 2.8e+02; Cmatches 0;
                                                                                                                                                                                                                                                                                  ĭ
                                                                                                                   English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A
                                                                                                                                                                                                                                                                                Kuwana
                                                                                                                                                                                                                                                                                  Nakamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                       and
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В
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                                                                                                          Query Match
Best Local S
Matches 5
                                                                                                                                                                                                                                                                  are introduced into animal cells and the transformant thus obtained is cultured for the prodn. of a chimmeric human Ab reacting with the ganglioside GM2. In contrast to mouse monoclonal Abs, the chimmeric human Abs will not cause anti-mouse Ig Ab prodn. in the patient's body but show a prolonged blood half-life, with a reduced frequency of adverse effects, so that it can be expected to be superior to mouse monoclonal Abs in the efficacy in the treatment of human cancer, for instance.
                                                                                                                                                                                                                    Mouse anti-GM2 monoclonal Ab KM-796 and KM-750 and rat KM-603 heavy and light chain sequences are given in AAQ45426-30. CDR regions for use in chimeric Abs are indicated in the
                                                                                                                                                                        Sequence
                                                                                                                                                                                                         Features Table.
                                             11 LLIWLP
                                                                           1 LLIWIP 6
                                                                                                                         Similarity
                                                                                                                                                                          128
                                               16
                                                                                                            Conservative
                                                                                                                                                                          AA;
                                                                                                                         94.1%;
83.3%;
Ψ
                                                                                                                         Score
Pred.
                                                                                                            Mismatches
                                                                                                                         32;
                                                                                                     DB 15; LC. 1.8e+02; O;
                                                                                                                                       Length 128
                                                                                                            Indels
                                                                                                            0
                                                                                                          Gaps
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0;

Q

888888<del>%</del>&

Search completed: January Job time : 27.5909 secs 2003, 15:28:35

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Minimum DB seq
Maximum DB seq
                                      Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                 Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                     Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                        OM protein - protein search, using sw model
                                                                                                                                                                                Searched:
                                                                                                                                   al number of hits satisfying chosen parameters:
                                                                           length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                 US-09-543-188A-3
                                                                                                                                                                                                                                                                                                                                                        January 3, 2003, 15:25:00; Search time 9.95455 Seconds (without alignments) 57.944 Million cell updates/sec
                                                                                                                                                                            283224 seqs, 96134422 residues
                                                                                                                                                                                                                   Gapop 10.0 ,
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GenCore version 5.1.3 (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                   Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Database

PIR\_73:\*
1: pir1::
2: pir2::
3: pir3::
4: pir4::

pir1:\*
pir2:\*
pir3:\*

### SUMMARIES

Result No.	Score	Query Match 1	Length I	DB	ID	Description
بر	34	100.0	367	2	F70036	capsular polysacch
2		•	402	٢	6597	nsport protei
ω	34	100.0	554	2	75	ש
4	34	80.	754	N	8504	probable LRR recep
U		٠	2452	۳	RNZQ2L	cted
6		100.0	2457	ν	T18492	prot
7		97.1	171	2	C45665	
8		97.1	304	2	S69034	bra
9		•	126	N	S40312	
10	32	94.1	200	N	G83834	
11		•	269	Ņ	T15500	hetical
7.2		•	100	Λ.	G82822	
L		•	542	Ν	T19862	hypothetical prote
14		91.2	114	N	800996	Ig kappa chain pre
1 U			115	\ \	SIUI46	kappa chain
10		•	111	N	· C	kappa chain
17		•	120	N	73	
			120	N	S06732	kappa chain
19		•	128	N	JL0073	kappa
20			131	_	KVMSM6	kappa
21			131	N	PH1226	kappa chain
22		•	131	2	S55027	light chain
23		•	131	Ν	G83872	pothetical pr
24			132	Н	KVMS32	kappa chai
25		٠	140	2	4	kappa chain
26		•	157	N	$\sim$	known proteir
27			229	N	-	hypothetical prote
28		•	280	ν	155577	a (IgG)
29	31	91.2	336	Ν	I48471	(IgG)

45	44	43	42	41	40	39	38	37	36	35 5	34	33	32	31	30
31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31
91.2	91.2	91'.2	91.2	91.2	91.2	91.2	91.2	91.2	91.2	91.2	91.2	91.2	91.2	91.2	91.2
741	512	500	443	443	431	404	396	396	396	374	365	349	349	349	344
2	N	N	N	N	N	N	N	N	_	1	N	N	N	N	2
A83271	T15669	AF2325	D64610	C71904	H84069	A46480	н86051	F91205	B65169	A39878	A48105	A81519	G72021	B86603	A41357
hypothetical prote	hypothetical prote	NADH dehydrogenase	dicarboxylate memb	anaerobic c4-dicar	hypothetical prote	Fc gamma (IgG) rec	2-module integral	2-module integral	multidrug resistan	Fc gamma (IgG) rec	probable M-factor	phospho-N-acetylmu	muramoyl-pentapept	muramoyl-pentapept	Fc gamma (IgG) rec

capsular polysaccharide biosynthesis homolog yveQ - Bacillus subtilis

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C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997
A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galiech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M. Roetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levlne, A.; Liu, H.; Masuda, S.; Mau, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, A.; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili A; Reference number: A69580; MUID: 98044033; PMID: 9384377
A. Status: Translation acid sequence of the Gram-positive bacterium Bacillus subtili A.; Accession: F70036
                                 transport protein homolog yycB - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: 565973; A70089
R:Ogasawara, N.; Nakai, S.; Yoshikawa, H.
DNA Res. 1, 1-14, 1994
A;Title: Systematic sequencing of the 180 kilobase region of the Bacillus subtilis ch A;Reference number: S65967; MUID:96051385; PMID:7584024
A;Accession: S65973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C:Accession: F70036
                                                                                                                                                                                                                                                                                                                                                                                                                S65973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:Z99121; GB:AL009126; NID:g2635827; PIDN:CAB15436.1; PID:e11861
A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-367 <KUN>
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37 LLIWIP 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LLIWIP 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 34; DB Pred. No. 64; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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Consortium, The Cold

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A;Cross references: EMBL:D26185; NID:g467326; PIDN:BAA05179.1; PID:g467333
A;Cross references: EMBL:D26185; NID:g467326; PIDN:BAA05179.1; PID:g467333
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1993
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1993
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1993
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1993
A;Note: the nucleotide sequence of the Gram-positive bacterium Bacillus subtilis.
A;Note: the nucleotide sequence of the Gram-positive bacterium Bacillus subtilis.
A;Cross references: EMBL:D26185; NID:g467326, 1997
A;Note: the nucleotide sequence of the Gram-positive bacterium Bacillus subtilis.
A;Cross references references references references not shown
A;Mitchary: nucleic acid sequence not shown; translation not shown
                         Ş
                                                                                                                                                 A;Description: involved in surface protein binding to the membrane via glycosyl-phosphata;Pathway: GPI-anchor biosynthesis
C;Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein
                                                                                                                                                                                                                                                                             A;Cross-references: GDB:9956843; OMIM:604122
A;Map position: 15q21-15q22
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:D42138; NID:g1552168; PIDN:BAA07709.1; PID:g1552169
A;Experimental source: cell line P39
A;Note: part of the genomic DNA was also sequenced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: S71751

9.TRKAhashi, M.; Inoue, N.; Ohishi, K.; Maeda, Y.; Nakamura, N.; Endo, Y.; Fujita, T.; To J. 15, 4254-4261, 1996

O J. 15, 4254-4261, 1996

A;Reference number: S71751; MUID:97015126; PMID:8861954

A;Accession: S71751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dolichyl-phosphate-mannose-glycolipid alpha-mannosyltransferase (EC 2.4.1.130) PIGB - hu. N.Alternate names: membrane protein PIG-B; phosphatidyl-inositol glycolipid biosynthesis
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A; Start codon: TTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-402 <KUN>
A;Cross-references: GB:Z99124; GB:AL009126; NID:g2636442;
A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                     A; Gene: GDB: PIGB
                                                                                                                                                                                                                                                                                                                                                                                    C;Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-554 <TAK>
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A; Residues: 1-402 <OGA>
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                                                                             Matches
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                         1 LLIWIP 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LLIWIP 6
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                                                                           Similarity 6; Conserv
                                                                           Conservative
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                                                                                               100.0%; Score 34; DB 100.0%; Pred. No. 94;
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Pred. No.
                                                                             Mismatches
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                                                                                                                                                                          predicted
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                                                                                                                            DB 2;
                                                                                                                                                                             <MMT>
                                                                           0;
                                                                                                                       Length 554;
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                                                                           0
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                                                                                                                                              hypothetical protein C0805w - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: Plasmodium DNA-directed RNA polymerase II large chain C;Keywords: DNA binding; nucleotidyltransferase; phosphoprotein; tanc F;68-84/Region: zinc finger CCHH motif F;2247-2384/Region: 7-residue repeats
                       A; Reference number: 218935
A; Accession: T18492
                                                                     R;Lawson, D.; Bowman, S.; Barrell, I submitted to the EMBL Data Library,
                                                                                                                            C; Accession: T18492
                                                                                                                                                                                                                              T18492
                                                                                                                                                                                                                                                      RESULT 6
                                                                                                                                                                                                                                                                                                                           В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;376/Binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X16561; NID:g9942; PIDN:CAA34560.1;
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A; Residues: 1-2452 <LIW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: S07485; A; Accession: S07485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Li, W.B.; Bzik, D.J.; Gu, H.; Tanaka, M.; Fox, B.A.; Inselburg, Nuccleic Acids Res. 17, 9621-9636, 1989.
A;Title: An enlarged largest subunit of Plasmodium falciparum RNA A;Reference number: S07485; MUID:90098832; PMID:2690004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jun-2000
C;Accession: S07485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA-directed RNA polymerase (EC 2.7.7.6) II large chain - malaria parasite (Plasmodiu C; Species: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
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A;Molecule type: DNA
A;Residues: 1-754 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable LRR receptor-like protein kinase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: AT4g03390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:NC_001268; NID:g7270209; PIDN:CAB77824.1; GSPDB:GN00140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title:
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nes 6; Conserv
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preliminary; translated
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  from GB/EMBL/DDBJ
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Pred. No. 3.9e+02;
Mismatches 0;
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Pred. No. 1.3e+02;
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A; Residues: 1-304 < PUL>
A; Cross-references: EMBL: U40829; NID: g1066476;
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C;Superfamily: rabbit adult-specific brush border protein
C;Keywords: intestine; transmembrane protein
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A; Residues: 1-171 <BOL>
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A; Note: C0805w
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A; Residues: 1-2457 <LAW>
                                                                                                                                                                                                                                    F;160-176/Domain:
                                                                                                                                                                                                                                                                                    A; Map position: 16R
                                                                                                                                                                                                                                                                                                                     A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                A; Gene: MIPS: YPR147c
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A; Accession: S69034
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                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                            Keywords: transmembrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pecies: Saccharomyces cerevisiae
Jate: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 19-Apr-2002
Accession: S69034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pecies: Oryctolagus cuniculus (domestic rabbit)
Date: 03-May-1994 #sequence_revision 03-May-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pable membrane protein YPR147c - yeast (Saccharomyces cerevisiae)
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                                                            <del>ب.</del>
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LLVWIP 36
                                                         LLIWIP 6
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                                                                                                                  Similarity 5; Conserved
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                                                                                                                  Conservative
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                                                                                                                                       97.1%;
83.3%;
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100.0%; P
tive 0;
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                                                                                                            Score 33; DB Pred. No. 81; 1; Mismatches
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Pred. No. 3.9e+02;
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47;
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                                                                                                                  Indels
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Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: G83834
                                                                                                                                                                                                                                                                                         RESULT 11
T15500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their
A;Reference number: $40312; MUID:94080891; PMID:8258341
A;Accession: $40312
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C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change
C;Accession: S40312
                       A; Molecule type: DNA
A; Residues: 1'-269 <N
                                                              A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                   submitted to the EMBL Data Library, March 1995
A;Description: The sequence of C. elegans cosmid C15B12
A;Reference number: Z18362
A;Accession: T15500
                                                                                                                                                                               R; Nhan,
                                                                                                                                                                                                 hypothetical protein C15B12.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #tey C;Accession: T15500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AP001512; GB:BA0000004; NID:g10174030; PIDN:BAB05198.1; GSPDB:GA;Experimental source: strain C-125
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A; Residues: 1-200 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein BH1479 [imported] - Bacillus halodurans (strain C-125) C; Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
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A; Residues: 1-126 < KLE>
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A;Cross-references: EMBL:U23529; NID:g746592; PID:g746594; PIDN:AAC46577.1; CESP:C15B
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83.3%;
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66.7%;
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Pred. No.
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Pred.
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A:Cross-references: GB:AE003884; GB:AE003849; NID:g9105127; PIDN:AAF83128.1; GSPDB:GN001
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; & Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, F. as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junquelra, M.L.; Kemper, E.L.; Kltajina, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigi Chado, M.A.; Madeira, M.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A.; Matchors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvai, R.S.; Vettore, A.L.; Zander, R.S.; Palada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Zander, R.S.; Palada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Zander, R.S.; Palada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Zander, R.S.; Palada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Zander, R.S.; Palada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Zander, R.S.; Palada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Zander, R.S.; Palada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Zander, R.S.; Palada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Zander, R.S.; Palada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Zander, R.S.; Palada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Zander, R.S.; Palada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Zander, R.S.; Palada, R.S.; Vertore, A.L.; Zander, R.S.; Palada, R.S.; Palada, R.
                                                                                                                                                                                 R;Hembry, C. submitted to the EMBL Data
                                                                                                                                                                                                                                               hypothetical protein C40C9.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 18-Feb-2000
C;Accession: T19862
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A; Residues:
          A; Molecule type: DNA
A; Residues: 1-542 <WIL>
                                                                                                               A; Reference number: A; Accession: T19862
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C; Superfamily: Caenorhabditis
                                                                        A; Status: preliminary; translated
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Nate: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 03-Jun-2002
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uperfamily: NADH dehydrogenase (ubiquinone) chain
uperfamily: NADH dehydrogenase (ubiquinone) chain
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83.3%;
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Pred. No.
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l; Mismatches
                                                                               from GB/EMBL/DDBJ
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1.1e+02;
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Biol. Chem. Hopper-Seyler 369, 601-607, 1988
A;Title: Two unusual human immunoglobulin V-kappa genes A;Reference number: S00996; MUID:89134397; PMID:2852016 A;Molecula turns.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
S00996
A;Introns: 17/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
E;1-20/Domain: signal sequence #status predicted <SIG>
F;21-115/Product: Ig kappa chain V region #status predicted <MAY
F;36-110/Domain: immunoglobulin homology <IMM>
F;36-110/Domain: immunoglobulin homology <IMM>
F;36-108/Disulfide bonds: #status predicted.
                                                                                                                                                                                                                                                                                  R:Straubinger, B.: Thiebe, R.: Huber, C.: Osterholzer, 1
Biol. Chem. Hoppe-Seyler 369, 601-607, 1988
A:Title: Two unusual human immunoglobulin V-Kappa genes
A:Reference number: S00996; MUID:89134397; PMID:2852016
A:Accession: S10146
                                                                                                                                                                    A;Note: this sequence was determined C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Keywords: heterotetramer; immunoglobulin F;1-19/Domain: signal sequence *status predicted * F;20-114/Product: Ig kappa chain V region *status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 23-Jul-1999
                                                                                                                                                                                          A;Cross-references: EMBL:M27751; NID:g185916; PIDN:AAA58913.1; PID:g185917 A;Note: this sequence was determined from the germline gene
                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-115 <S
                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession: S10146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;42-107/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Introns: 16/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:M27750; NID:g185914; PIDN:AAA58912.1; PID:g553479 A;Note: this sequence was determined from the germline gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-114 <STR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: S00996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Introns: 11/3; 69/3; 123/2; 173/3; 216/1; 248/1; 279/1; 314/1; 350/3; 430/1; 464/1; C; Superfamily: acetylcholine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Map position: X
A; Introns: 11/3; 69/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: CESP:C40C9.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:Z70266; PIDN:CAA94206.1; GSPDB:GN00028; CESP:C40C9 A;Experimental source: clone C40C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig kappa chain precursor V region (Al4) - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig kappa chain precursor V region (AlO) - human (fragment)
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nes 5; Conserv
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4; Conserv
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66.7%;
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83.3%;
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Pred. No.
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Pred. No.
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Query Match
DestLocal Similarity 66.7%; Pred. No. 74;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0; ...

QV 11LIMIP 6
Db 11 LLLWP 16

Search completed: January 3, 2003, 15:33:15
Job time: 11.9545 secs 3, 2003, 15:33:15
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Match
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YGR1_YEAST
NU1M_POLOR
MTF1_SACKL
Y567_HELPY
Y567_HELPJ
CEMA_NEPOL
GAC3_HUMAN
GAC3_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                            MAP3_SCHPO
FCG1_HUMAN
EMRD_ECOLI
FCG1_MOUSE
DCUA_HELPJ
DCUA_HELPY
                                                                                                                                                                                                                KV3H_HUMAN
KV3L_HUMAN
KV3M_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O56A_DROME
RPB1_PLAFD
BB19_RABIT
                                                                                                                                                                        Y4QB_RHISN
PLSC_HAEIN
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cillus.  cillus.  of the Bacillus  igin.";  Alloni G.,  Borchert S.,  nell S.C. Bron S.,  v. Carter N.M.,  D. Emmerson P.T.,  Foulger D.,  A. Galleron N.,  Grandi G.,  Kumano M., Klein C.,  Kumano M., Klein C.,  Kai S., Noback M.,  Bazarevic V.,  Medigue C.,  kai S., Noback M.,  ga B., Park S.H.,  Prescott A.M.,  Prescott A.M.,  Rey M., Reynolds S.,  Coffone F.,  Shin B.S., Soldo B.,  Takemaru K.,  Tognoni A.,  Vassarotti A.,  Vassarotti A.,  Tognoni A.,  Vassarotti A.,  Pogger T.,  enegger T.,  a H., Danchin A.;  e bacterium Bacillus	P28473 rattus norv Q09226 caenorhabdi Q10286 schizosacch P45848 escherichia P58721 salmonella P58720 escherichia Q9acp0 salmonella P45800 escherichia P45800 escherichia P45800 escherichia P45800 organis rattus norv Q92887 homo sapien Q26887 homo sapien Q26889 mus musculu

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RESULT 2
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Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
A Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
A Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
B George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
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A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
A Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
A Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
A Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
A Ballew R.M., Basu A., Baxendale J., Bayrakteroglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendale J., Bayrakteroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
A Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
A Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
A Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
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MEDLINE-20196006;
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Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Molson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Syliskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RI Science 287:2185-2195(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical Olfaction; M
                                                                        SEQUENCE
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between the Swiss Institute of Bioinformatics and the EMBL
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-!- FUNCTION: PROBABLE ROLE IN THE ODORANT RESPONSE, BE
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pean Bioinformatics Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                profit institutions as long as its content
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                                                                        MW,
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                                                                                            7 (POTENTIAL)
CYTOPLASMIC (I
                                                                                                                       CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
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Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
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                                              DOMAIN
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                                                                                                                                                                                                                                      EMBL; X16561; CAA34560.1; -.
PIR; S07485; RNZQ2L.
Interpro; IPR000684; RNA_poll_A.
Interpro; IPR000722; RNA_pol_A2.
Interpro; IPR002879; RNA_pol_A2.
                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                             DNA-binding;
ZN_FING
                                                                                                                                                                                                                                   Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic Acids Res. 17:9621-9636(1989).
-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
                                                                                        DNA_BIND
                                                                                                     DOMAIN
                                                                                                                    DOMAIN
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Eukaryota; Alveolata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA-directed
                                                                          DOMAIN
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                                                                                                                                                                                         Transferase;
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                                                                                                                                                                                                        PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W.B., Bzik D.J., Gu H., Tanaka M., Fox B.A., Inselburg n enlarged largest subunit of Plasmodium falciparum RNA defines conserved and variable RNA polymerase domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 III FOR 5S AND TRNA GENES.
SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (RNA)(N).
SUBUNIT: EACH CLASS OF RNA POLYMERASE IS ASSEMBLED THE DIFFERENT POLYPEPTIDES. THIS POLYPEPTIDE IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBSTRATES.

CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
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MISCELANDOUS: THREE DISTINCT ZINC-CONTAINING RN
FOUND IN BUKARYOTIC NUCLEI: POLYMERASE I FOR THE
PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Nuclear.
PTM: THE TANDEM 7 RESIDUES REPEATS CAN BE HIGHLY PHOSPHORYLATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TWELVE DIFFERENT POLYPEPTIDES. COMPONENT OF RNA POLYMERASE II.
                                                                                                                                  PF00623; RNA_PO1_A2; 1.

PF01854; RNA_PO1_A2; 1.

FF01854; RNA_POL_II_REPEAT; 9.

ITE; PS00115; RNA_POL_II_REPEAT; 9.

Sferase; DNA-directed RNA polymerase; Transcription; sferase; DNA-directed RNA polymerase; Transcription; finge conding; Nuclear protein; Phosphorylation; Zinc-finge C2H2-TYPE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE
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(Rel. 37, Last ann
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37, Last annotation update)
polymerase II largest subunit
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Apicomplexa;
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ASP/GLU-RICH (HIGHLY ACIDIC).
6 X TANDEM REPEATS OF [YIV]-D(3,4).
ASP/GLU-RICH (HIGHLY ACIDIC).
ASP/GLU-RICH (HIGHLY ACIDIC).
ASP/GLU-RICH (HIGHLY ACIDIC).
                                                                          POLY-ASN.
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                                                                                                                   LEUCINE-ZIPPER
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Haemosporida;
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AND POLYMERASE
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RESULT 5
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21-JUL-1986
21-JUL-1986
15-JUL-1999
                              KV3I_MOUSE P01661;
                                                                                                                                                                                    TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                  Signal; Transmembrane.
SIGNAL 1 21
CHAIN 22 171
                                                                                                                                                                                                                                                                                                  modified and this statement
                                                                                                                                                                                                                                                                                                                                                                      Isolation of cognate cDNAs and characterization of a novel brush border protein with esterase and phospholipase activity.";
J. Biol. Chem. 268:12901-12911(1993).
-i- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-i- TISSUE SPECIFICITY: INTESTINE.
-i- DEVELOPMENTAL STAGE: EXPRESSED IN THE INTESTINE OF ADULT BUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1994
15-JUL-1998
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01-FEB-1994
                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                             EMBL;
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                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                Boll W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brush border
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                                                                                                     1 LLIWIP
                                                                                           63 LLIWVP
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                                                                                                                                                                                                                                                                                                                                                                 BABY RABBITS.
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49
88
131
171 AA;
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83.3%;
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Last sequence up
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Pred. No.
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                                                                                                                                                                                                                    BRUSH BORDER
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                                       131
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Blochemistry 17:2392-2400(1978).
                                                                                P01658;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-79012520; runner M.;
MCKean D.J., Bell M., Potter M.;
"Mechanisms of antibody diversity: multiple genes related mouse kappa variable regions.";
related mouse kappa variable 75:3913-3917(1978).
                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00047; ig; 1. SMART; SM00406; IGv; Immunoglobulin V regi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=73140225; PubMed=4691517;
MCKean D.J., Potter M., Hood L.E.;
Mouse immunoglobulin chains. Pattern of sequence
"Mouse immunoglobulin chains."
kappa chains with limited sequence differences.";
Burstein
          SEQUENCE OF 1-37.
MEDLINE=78235887; PubMed=98179;
                                                                   Snw
                                                                                                                        KV3F_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci
PIR; A01935; KVMSM6.
HSSP; P01679; 2FBJ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                      NCBI_TaxID=10090;
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                                                                           kappa chain
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                                                                musculus (Mouse)
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21
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Schechter I.;
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                                                                          V-III region MOPC
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                                                                                                                         STANDARD;
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                                               Chordata;
Rodentia;
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Rodentia;
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66.7%;
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Pred.
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FRAMEWORK-2.
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                                                                                                                                                                                                                                                                            FRAMEWORK - 4
                                              Craniata; Ver
Sciurognathi;
                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; E
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                D212EC9F08DC880A CRC64;
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                                                                                   update)
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33;
                                                       Vertebrata;
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                                               Muridae;
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                                                       Euteleostomi;
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                                                Murinae;
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RESULT
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Best Local :
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P87250;
15-JUL-1998 (Rel. 3
15-JUL-1998 (Rel. 3
30-MAY-2000 (Rel. 3
Gene Expr. 6:219-230(1996).

Gene Expr. 6:219-230(1996).

1- FUNCTION: ESSENTIAL FOR MITOCHONDRIAL REPLICATION AND TRANSCRIPTION. CONFERS SELECTIVE PROMOTER RECOGNITION ON SUBUNIT OF THE YEAST MITOCHONDRIAL RNA POLYMERASE. INTERADA IN A NON-SPECIFIC MANNER (BY SIMILARITY).

1- SUBCELLULAR LOCATION: Mitochondrial (By similarity).

1- SIMILARITY: FANIT SIMILARITY WITH THE T4 GENE 32 PRODUCT BACTERIAL SIGMA FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID NON_TER
                                                                                             Carrodeguas J.A., Yun S. "Functional conservation
                                                                                                                                               Saccharomycetales;
NCBI_TaxID=28985;
                                                                                                                                                                   Kluyveromyces lactis (Yeast).
Eukaryota; Fungi; Ascomycota;
                                                                                                                                                                                                                                                                          KLULA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                  divergence."
                                                                                                                SEQUENCE FROM N.A. MEDLINE=97339478;
                                                                                                                                                                                          MTF1.
                                                                                                                                                                                                             Mitochondrial replication
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SMART; SM00406; IG;
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MEDLINE=73140224; F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Primary structures of N-terminal extra peptide segments linked the variable and constant regions of immunoglobulin light chain precursors: implications on the organization and controlled expression of immunoglobulin genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
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Pro; IPR003006;
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immunoglobulin chains.
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NEOUS: THE PARTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   f immunoglobulin genes.";
17:2392-2400(1978).
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39, Last annotation updat
                                                                                                                   PubMed=9196077;
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                                                                                                                                                                                                            protein MTF1
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                                                                                             yeast
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BY SIMILARI
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FRAMEWORK-1
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                                                                                                                                                          Saccharomycotina; Saccharomycetes; Setaceae; Kluyveromyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Partial amino acid
                                                                                                                                                                                                                                                                 PRT;
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                                                                                                        Clayton D.A.,
                                                                                                                                                                                                             (Mitochondrial
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Matches
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                                                                                                                                                                                       MEDLINE-20330349; PubMed-10871362; Shirai M., Hirakawa H., Kinoto M., Tabuchi M., Kishi F., Ouchi K Shirai M., Ishii K., Hattori M., Kuhara S., Nakazawa T.; "Comparison of whole genome sequences of Chlamydia pneumoniae JI from Japan and CWL029 from USA."; Nucleic Acids Res. 28:2311-2314 (2000).

-i- FUNCTION: FIRST STEP OF THE LIPID CYCLE REACTIONS IN THE BIOSYNTHESIS OF THE CELL WALL PEPTIDOGLYCAN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S. Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S. Eisen J., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MRAY_CHLPN STANDARD; PRT; 349 AA. 09Z706; 09J512; 30-MAY-2000 (Rel. 39, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Phospho-N-acetylmuramoyl-pentapeptide-transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nat.
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kalman S., Mitchell W., Marathe R., I
Olinger L., Grinwood J., Davis R.W.,
"Comparative genomes of Chlamydia pne
Nat. Genet. 21:385-389(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murnac-pentapeptide phosphotransferase).
MRAY OR CPN0900 OR CP0966.
Chlamydia pneumoniae (Chlamydophila pneu
Bacteria; Chlamydiales; Chlamydiaceae; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mitochondrion; DNA SEQUENCE 335 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U81620; AAC49739.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20150255; PubMed=10684935;
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MEDLINE=99206606; PubMed=10192388;
MEDLINE=9920606; PubMed=10192388;
Marathe R., Lammel C., Fan J., Hyman R.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-J138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pneumoniae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequences of Chlamydia trachomatis MoPn and pneumoniae AR39.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic Acids
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                                                                                                  CATALYTIC ACTIVITY: UDP-N-acetylmuramoyl-L-alanyl-D-glutamyl-L-lysyl-D-alanyl-D-alanine + undecaprenyl phosphate = UMP + N-acetylmuramoyl-L-alanyl-D-glutamyl-L-lysyl-D-alanyl-D-alanine-
  SIMILARITY: BELONGS
                                SUBCELLULAR
                                                    PATHWAY: Peptidoglycan biosynthesis.
                                                                              diphosphoundecaprenol
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                                LOCATION:
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66.7%;
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  TO
Integral membrane protein (By similarity).
O THE GLYCOSYLTRANSFERASE FAMILY 4. MRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2;
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79;
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91 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
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                                                                                                                                                                                                                                                                                                                                                             Ouchi K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA-binding
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RESULT 9
MAP3_SCHPO
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Best Local
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P31397;
01-JUL-1993
01-JUL-1993
15-JUN-2002
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TRANSMEM
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TRANSMEM
                                                                                                                                                                            Schizosaccharomyces pombe (Fission Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales; Schizosacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE001670; AAD19038.1; -.
EMBL; AE002254; AAF38746.1; -.
EMBL; AE002248; BAA99108.1; -.
TIGR; CP0966; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-s
       MEDLINE=21848401; PubMed=11859360; Wood V., Gwilliam R., Rajandream M Sgouros J., Peat N., Hayles J., Ba
                                                                                                                                                       Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                      Tanaka K.,
                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                            MAP3 OR SPAC3F10.10C.
                                                                                                                                                                                                                     Pheromone M-factor receptor.
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00953;
                                                   SEQUENCE
                                                                                           "Schizosaccharomyces
                                                                                                               MEDLINE=93109361; PubMed=8380233;
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4; Conserv
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                                                  FROM N
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Brown D.,
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                                                                       Biol. 13:80-88(1993).
                                                                                                     Davey J.,
                                                                                                                                                                                                                                                                                                                                                 σ
                                                                                                                                                                                                                               (Rel. 26, Last sequence up
(Rel. 41, Last annotation
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165
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278
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                                                                                                                                                                                                                                                                         STANDARD;
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89
111
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185
217
248
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272
298
347
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66.7%;
, Rajandream M.A., Lyne M., Lyne R., Stewart Hayles J., Baker S., Basham D., Bowman S., Brown S., Chillingworth T., Churcher C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                              38589
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                                                                                          pombe map3+
                                                                                                      Imai Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell
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S -> A (IN REF. 1).
6CAA9283C594A88B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                      ssion yeast).
Schizosaccharomycetes;
                                                                                                      Yamamoto M.;
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                                                                                          encodes the putative M-factor
                                                                                                                                                                                                                                         update)
                                                                                                                                                                                                                                                                         365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                               DB
82;
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                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                        Length 349;
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MBL outstation -
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JECG1_HUMAN

D FCG1_HUMAN

C P12314; P12315;

JT 01-CCT-1989 (Rel. 12, Created)

DT 01-CCT-2002 (Rel. 41, Last sequence update)

DE High affinity immunoglobulin gamma Fc receptor I pre

RI) (FCRI) (IGG Fc receptor I) (CD64).
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FCG1_HUMAN
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RA Holroyd S., Jones L., Jones M., Leather S., McDonald S., McLean J.,

RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,

RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,

RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

RA Gabel C., Fuchs M., Filtzc C., Holzer E., Moostl D., Hilbert H.,

RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,

RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,

Cerrutti L., Lowe T., McComble W.R., Paulsen I., Potashkin J.,

Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;

"The genome sequence of Schizosaccharomyces pombe.";

RL Nature 415:871-880(2002).

RL Nature 415:871-880, Seery D., Barrell B.G., Nurse P.;

"The genome sequence of Schizosaccharomyces pombe.";

RC PACTOR OF S. POMBE, M-FACTOR SIGNALING ALONE MAY BE SUFFICIENT.

CC ---- EUGCION: RECEPTOR FOR THE PEDTIDE PHEROMONE M-FACTOR, A MATING

CC ---- SUBCELLUIAR LOCATION: Integaral membrane portein
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Best Local S
Matches 4
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D10933; BAA01727.1; -. EMBL; 269369; CAA93308.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THE CELL, NUTRITIONAL CONDITIONS AND PHEROMONE SIGNALING. SIMILARITY: BELONGS TO FAMILY 4 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Integral membrane protein.
INDUCTION: BY AT LEAST 3 TYPES OF REGULATION: THE MATING-TYPE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A48105; A48105.
rPro; IPR001499; STE3_GPCR.
; PF02076; STE3; 1.
smembrane; G-protein couple
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s M., Connor R
s S., Goble A.
d S., Hornsby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s requires a license agreement (Some an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                      4
                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                  299
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Goble A., Hamlin N
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66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coupled
                                                                                                                                                                                                                                                                                                                                    Score 31; DB Pred. No. 85; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
POTENTIAL.
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306A022FA7DCFEF7 CRC64;
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85;
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                                                                                  precursor (Fc-gamma
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DISULFID
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SMART; SM00410; IG_iro.,
SMART; SM00408; IGc2; 1.
SMART; SM00408; IGc2; 1.
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PIR;
PIR;
PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- ALTERNATIVE PRODUCTS: 2 ISOFORNS; A (SHOWN HERE) AND I PRODUCED BY ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: MONOCYTE/MACROPHAGE-SPECICIC.
-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
-!- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DO)
                                                   CARBOHYD
                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complementary DNAs.";
Science 243:378-381(1989).
-!- FUNCTION: BINDS TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=89098339; Allen J.M., Seed B
   CARBOHYD
                CARBOHYD
                                  CARBOHYD
                                                                     CARBOHYD
                                                                                                          CARBOHYD
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                                                                                                                                                                                                                                                                       DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Isolation and expression of functional high-affinity complementary DNAs.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genew; HGNC:3613; FCGR1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Allen J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-89100284;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Nucleotide sequence of three cDNAs for the receptor (FCRI).";
                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor (FcRI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; S03018; S03018.
; S03019; S03019.
; A41357; A41357.
; B41357; B41357.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DATABASE: NAME=PROW: NOTE=CD guide CD64 entry;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd64.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AFFINITY RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146760;
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                                                                                                                                                                                                                                                                                                                                                                                                                        IPR003006; Ig_MHC.
IPR003598; Ig_c2.
IPR003600; Ig_like.
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16:11824-11824(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FC
                                                                                  POTENTIAL.

CYTOPLASMIC (POTENTIAL).

IG-LIKE C2-TYPE DOMAIN 1.

IG-LIKE C2-TYPE DOMAIN 3.

IG-LIKE C2-TYPE DOMAIN 3.

BY SIMILARITY.

BY SIMILARITY.
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                                                   N-LINKED
                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                         Transmembrane; Glycoprotein; Signal; Alternative splicing; Polymorphism.
                                                                                                                                                                                                                                                                                                        AFFINITY IMMUNOGLOBULIN
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            (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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L outstation -
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Best Local S
Matches 4
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                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
SEQUENCE
                TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                 Burland V.D., Plunkett G. III, Daniels D.L., Blattner F.R.; "DNA sequence and analysis of 136 kilobases of the Escherichia coli genome: organizational symmetry around the origin of replication.";
                                       Transport;
                                                           Pfam; PF00083; sugar_tr; 1.
TIGRFAMs; TIGR00880; 2_A_01_02; 1.
                                                                                                             EcoGene; EG11693;
                                                                                                                          EMBL;
                                                                                                                                                          or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Multidrug
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16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P31442;
01-JUL-1993
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                                                                                       InterPro;
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                                                                                                                                                                                                                                                                                                     ENERGY SHOCK ADAPTATIVE RESPONSE. SUBCELLULAR LOCATION: Integral membrane
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                                                                                                                         AE000445;
                                                                                                                                    L10328; AAA62025.1; ALT_INIT
                                                                                                                                                                                                                                                                     THE DRUG
                                                                                                                                                                                                                                                                                                                                                                                                                                       En-94059107; PubMed-8240355;

tskaya V., Schloseer M.J., Fan N.Y., Lewis K.;

coli gene emrD is involved in adaptation to low energy shock.";

m. Biophys. Res. Commun. 196:803-809(1993).
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Transmembrane;
9 29
47 67
74 94
96 116
                                                                                 IPR004734; Drug_resist.
IPR003662; sub_transporter.
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01 (Rel. 40, Last annotation updat resistance protein D.
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374 i
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                                                                                                                         AAC76696.1;
                                                                                                                                                                                                                                                                 BELONGS TO THE MAJOR FACILITATOR FAMILY RESISTANCE TRANSLOCASE FAMILY). BELONGS
                                                                                                            emrD.
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                                                 Inner membrane;
                                                                                                                       ALT_INIT.
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Pred. No.
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S -> T (IN REF. 1;
2C2AA8103ECF16E6
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N -> V.
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                POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   subdivision; Enterobacteriaceae;
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T.
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                                                 Complete proteome
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                                                                                                                                                                                                                                                                                                      protein.
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CRC64;
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BELONGS TO THE
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FCG1_MOUSE
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15-JUN-2002 (Rel. 41, Last annotation update)
High affinity immunoglobulin gamma FC recep
RI) (FCRI) (IGG FC receptor I)
                                                                                                                   the European Bioinformatics Institute. Thuse by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
      InterPro; IPR003006; Ig_MHC.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003500; Ig_like
Pfam; PF00047; ig; 3.
                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1992 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FCG1_MOUSE P26151;
                                            MGD; MGI:95498; Fcgr1.
                                                                                 EMBL; M31314; AAA40056.1; -.
                                                                                                                                                                                                                                                                                  MEDLINE=92166399;
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                        receptor for IgG.
                                                                                                                                                                                                                                                                                                                                                  MEDLINE=90111035;
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                    FCGR1 OR FCG1.
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                                                              A43511;
A46480;
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                                                       P12319;
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5; Conser
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nilarity 83.3%;
Conservative
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A46480.
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n N., Tate B., McK
ng and expression
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22,
41,
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              Ig_c2.
Ig_like.
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342339DC7265A30B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor I precursor (FC-gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
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mouse high affinity Fc
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                                                       the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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SEQUENCE
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Smith D.R., Noonan B., Guild B.C., deJonge B.L., C
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylo
   EMBL; AE001498; AAD06239.1;
InterPro; IPR004668; Dcu.
Pfam; PF03605; Dcu; 1.
TIGRFAMs; TIGR00770; Dcu; 1
                                                                                                                                                                                                  "Genomic sequence comparison of two unrelated gastric pathogen Helicobacter pylori."; Nature 397:176-180(1999).
                                                                                                                                                                                                                                                                                                                                           Helicobacter pylori J99 (Campylobacter pylori J99)
Bacteria; Proteobacteria; epsilon subdivision; Hel
                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Creat
16-OCT-2001 (Rel. 40, Last
16-OCT-2001 (Rel. 40, Last
Anaerobic C4-dicarboxylate
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                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=85963;
                                                                                                                                                                                                                                                                                                                                      Helicobacter
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                                                                                                                                                         THE PERIPLASM ACROSS THE INNER MEMBRANE SUBCELLULAR LOCATION: Integral membrane SIMILARITY: BELONGS TO THE DCUA / DCUB (
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5 LLLWVP 21
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                                                                                                              SWISS-PROT entry is copyright. It is produced through a deen the Swiss Institute of Bioinformatics and the EMBL
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66.7%;
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CYTOPLASMIC (POTENTIAL).

IG-LIKE C2-TYPE DOMAIN 1

IG-LIKE C2-TYPE DOMAIN 2

IG-LIKE C2-TYPE DOMAIN 3

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Taylor D.E., Vovis
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RESULT 14
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Matches 4
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STRAIN=26695 / ATCC 700392;

MEDLINE=97394467; PubMed=9252185;

MEDLINE=97394467; PubMed=9252185;

Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,

Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty

Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,

Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,

McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,

McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,

Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley C.

Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Walthey

Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Walthey

Haves W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
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Anaerobic C4-dicarboxylate
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                                                                                                                                             pylori.
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THE PERIPLASM ACROSS THE INNER MEMBRANE (BY
SUBCELLULAR LOCATION: Integral membrane pro
SIMILARITY: BELONGS TO THE DCUA / DCUB (TC
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Transport; Transmembrane; Inner membrane; Complete proteome.

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                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
                                   EMBL; X01668; -; NOT_ANNOTATED_CDS PIR; A01900; K3HUVG. HSSP; P80362; 1WTL.
                                                                                                                                                                                within the VK locus.";
Nucleic Acids Res. 12:9229-9236(1984).
                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=85087932;
                                                                                                                                                                                                                                                        NCBI_TaxID=9606; [1]
                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                 13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-UIL-1999 (Rel. 38, Last annotation update)
15 kappa chain V-III region VG precursor (Fragment).
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'Immunoglobulin genes of different subgroups are interdigitated
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4; Conserv
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11 LLLWLP 16
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77
109
                             Conservative
                                                          ΑA;
                                                                                                                                           V region; Signal.
                                                                                                                                                   IGv; 1.
                                                                               108
115
                                                          12575 MW;
                                   88.2%;
66.7%;
                                    Score 30;
Pred. No.
                                                                       COMPLEMENTARITY-DETERMINING-3
BY SIMILARITY
                                                                                       COMPLEMENTARITY-DETERMINING-2. FRAMEWORK-3.
                                                                                                       FRAMEWORK-2
                                                                                                             COMPLEMENTARITY - DETERMINING - 1.
                                                                                                                     IG KAPPA CHAIN V-III REGION VG FRAMEWORK-1.
                                                         2DE47CDA3A17D555 CRC64;
                             Mismatches
                                  DB
45;
                                            1;
                                          Length 115
                             Indels
                             0
                             Gaps
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0;

Search completed: January 3, 2003, 15:29:19 Job time: 6.18182 secs

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Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   earched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       al number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                         Score
                                                                                                                                                                                                                                                                                                                  SPTREMBL_21:*

1: sp_archea:*
2: sp_bacteria
3: sp_fungl:*
4: sp_human:*
5: sp_inverteb:
6: sp_mammal:*
7: sp_mhc:*
8: sp_organel:
9: sp_plant:*
10: sp_plant:*
11: sp_rodent:
12: sp_virus:*
13: sp_verteb:*
14: sp_unclass
15: sp_verteb:*
16: sp_bacteri:
16: sp_archeap
17: sp_archeap
                                                                                                                                                                                                       Query
Match
100.0
100.0
100.0
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34
1 LLIWIP 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_archea:*
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sp_archeap:*
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16
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17
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                                  Q9NFS8
Q92521
Q8WVN7
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Q77375
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Q95W5
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                               006522 saccharomyc

098k16 rhizobium 1

09kzh9 streptomyce

0936u1 pseudomonas

005611 pseudomonas
                                                                                           Q8wvn7 homo sapien
Q9zqz2 arabidopsis
O77375 plasmodium
Q985w5 rhizobium 1
Q8ttc2 methanosarc
                                                                                                                                                      Q9nfs8 plasmodium
P71056 bacillus su
Q92521 homo sapien
                                                                                                                                                                                                       Description
        Q9kcu0 bacillus ha
Q9rkx7 streptomyce
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Q61468 mus musculu	Q61468	11	625	-	31	15
Q18267 caenorhabdi	Q18267	5	521		31	14
Q8ypn6 anabaena sp	Q8YPN6	16	500		31	ω.
-	Q9N983	ហ	494	٠	31	12
Q9k7k1 bacillus ha	Q9K7K1	16	431		31	Ë
1 esci	Q8X541	16	396		31	0
homo	Q92495	4	375		31	39
Q92663 homo sapien	Q92663	4	374	٠	31	88
maca	Q8SPW5	σ	357		31	37
2 mus	Q8R142	11	330	91.2	31	36
ÖΠO	095100	4	301		31	35
homo	Q9UGN4	4	299		31	34
homo	Q9UBK4	4	299		31	ω
homo	Q9нD97	4	298		31	3
Q92637 homo sapien	Q92637	4	280		31	3
caen	Q19308	ഗ	229		31	30
Q9umt0 homo sapien	Q9UMTO	4	186		31	
	Q8VD57	1	159		31	8
Q9c8r7 arabidopsis	Q9C8R7	10	157		31	
	Q98LW8	16	150		31	
1 bac	Q9KBZ1	16	131		31	
homo	Q9UMS9	4	103		31	
homo	Q9POF3	4	100		31	
	Q9DTD8	12	3011		32	
Q8s191 oryza sativ	Q8S191	10	902		32	21
Q18556 caenorhabdi	Q18556	ហ	542		32	
Q9pgi3 xylella fas	Q9PGI3	16	501	94.1	32	19
bactero	Q8VTB2	2	479		32	8
Q8w2p6 oryza sativ	Q8W2P6	10	382	94.1	32	١7

## ALIGNMENTS

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RESULT 1
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                                                                                                                                                                               Query Match
Best Local
                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                  "A study of selected Plasmodium yoelii messengers RNAs during hepatocyte infection.";
Mol. Biochem. Parasitol. 111:31-39(2000).
EMBL; AJ271478; CAB70097.1; -.
InterPro; IPR000722; RNA_pol_A.
Pfam; PF00623; RNA_pol_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium yoelii.
Eukaryota; Alveolata;
NCBI_TaxID=5861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O9NFS8:
01-OCT-2000 (TrEMBLrel. 15, Created)
01-DCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nivez M.P., Achbarou A., Bienvenu J.D., Mazier D., Doerig C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=265BY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNA polymerase II (Fragment). RNAPOLII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9NFS8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vaquero C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20542027; PubMed=11087914;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                             Local Similarity
66 LLIWIP 71
                                                                    1 LLIWIP 6
                                                                                                                                                                                                                                                                                      157
157 AA;
                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                157
                                                                                                                                                                                                                                                                                          18667 MW;
                                                                                                                                                                           100.0%; Score 34; DB 100.0%; Pred. No. 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                          79E0EA86CFEAF5CA CRC64;
                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157
                                                                                                                                                                                                                  DB 5; Length 157;
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RESULT P71056

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RX MEDLINE=98044033; PubMed=9384377;
RX MEDLINE=98044033; PubMed=9384377;
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Choi S.K., Codani J.J., Connerton I.E., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.E., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.E., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.E., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.E., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Brilich S.D., Emmerson P.T.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Hilbert H., Holsappel S., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Kurita K., Lapidus A., Lardinols S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinols S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinols S., Lauber J., Lazarevic V.,
RA Noone D., O'Reilly M., Ogawa K., Moerst D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Parecan E., Pujic P., Purnelle B., Rapport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Secon E., Takagi T., Takahashi H., Takemaru K.,
RA Secon E., Wiphat A., Yanamoto H., Yamane Y., Yasmaru K.,
Takeuchi M., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A.,
Tognoni A.,
Tognoni A., Yata K.,
The Complete genome sequence of the gram-positive bacterium Bacillus
                                                                                                                                                                      Query Match
Best Local
                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                     Kunst F., Ogasawara N., Yoshikawa H., Danchin Submitted (MOV-1997) to the EMBL/GenBank/DDBJ EMBL; Z71928; CA896474.1; -
EMBL; Z94043; CABB8029.1; -
EMBL; Z99121; CAB15436.1; -
                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The complete genome sequence subtilis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes;
Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus subtilis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P71056 PRELIMINARY;
P71056, 008175;
01-FEB-1997 (TrEMBLrel. 02,
01-FEB-1997 (TrEMBLrel. 02,
01-MAR-2002 (TIEMBLIEL. 20,
                                                                                                                                                                                                                                                                                                     Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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37 LLIWIP 42
                                                                          1 LLIWIP 6
                                                                                                                                        Similarity
6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (APR-1997)
                                                                                                                                                                                                                                                              al protein; Complete
367 AA; 42554 MW;
                                                                                                                                            Conservative
                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ., Chapal N., Guiseppi A., Haiech J., Denizot F.; to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ç
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Last sequence update)
Last annotation updat
                                                                                                                                                               Score 34; DB 16;
Pred. No. 1.2e+02;
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88D37986AFD9C9C6
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                                                                                                                                                                                                                                                                                                                                                                                                                          A.;
databases
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RESULT 5
Q9ZQZ2
ID Q9ZQ
AC Q9ZQ
DT 01-M
DT 01-M
DT 01-M
DT 01-M
DT 11-M
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Q8WVN7
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Q92521
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Best Local Similarity
Matches 6; Conserv
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Best Local :
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                      Q9ZQZ2
Q9ZQZ2;
Q1-MAY-1999
Q1-MAY-1999
Q1-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q92521
Q92521;
Q1-FEB-1997
Q1-FEB-1997
Q1-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                     OBWVN7
OBWVN7; PRELIMINARY;
O1-MAR-2002 (TrEMBLrel. 20,
O1-MAR-2002 (TrEMBLrel. 20,
O1-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                          Strausberg R.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC017711; AAH17711.1; ~. SEQUENCE 554 AA; 64957 MW; E778418C02A27488 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE=97015126; PubMed=8861954;
Takahashi M., Inoue N., Ohishi K., Maeda Y., Nakamura N., Endo Y.,
Fujita T., Takeda J., Kinoshita T.;
"PIG-B, a membrane protein of the endoplasmic reticulum with a large lumenal domain, is involved in transferring the third mannose of the GPI anchor.":
                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Ve
Mammalia; Eutheria; Primates; Catarrhini;
             Putative LRR
                                                                                                                                                                                                                                                                           TISSUE-PROSTATE;
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                            Phosphatidylinositol glycan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBO J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GPI anchor.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
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like protein
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6; Conserv
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                      (TrEMBLrel. 10, 17 (TrEMBLrel. 10, 20) (TrEMBLrel. 20, 20)
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                                                                       PRELIMINARY;
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kinase).
             receptor-linked
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Last annotation update)
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                                                                                                                                                                                           Score 34; DB 4;
Pred. No. 1.8e+02;
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Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi;
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             (Putative
                      update)
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            LRR receptor-
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Best Local
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Submitted (MAR-2000) to the EMBL/GenBank/D
EMBL; AC005275; AAD14467.1; -.
EMBL; AL161496; CAB77824.1; -.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR003592; LRR_out.
InterPro; IPR003592; LRR_out.
InterPro; IPR002965; P_rich_extensn.
Pfam; PF00560; LRR; 5.
Pfam; PF00069; pkinase; 1.
PRINTS; PR01217; PRTCHEXTENSN.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00370; LRR; 4.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
SMART; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                           Bowman S., Lawson D., Basham D., Brown D., Chillingworth T., Churcher C.M., Craig A., Davies R., Devlin K., Feltwell T., Gentles S., Gwilliam R., Hamlin N., Harris D., Holroyd S., Hornsby Horrocks P., Jagels K., Jassal B., Kyes S., McLean J., Moule S., Mungall K., Murphy L., Oliver K., Quail M.A., Rajandream M.-A., Rutter S., Skelton J., Squares R., Squares S., Sulston J.E., Whitehead S., Woodward J.R., Newbold C., Barrell B.G., Whitehead S., Woodward J.R., Newbold C., Barrell B.G.,
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Arabidopsis thaliana (Wouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheopspermatophyta; Magnoliophyta; eudicotyledons; core eudicots; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                        STRAIN=3D7;
MEDLINE=99376085;
                                                                                                                                                                                                                         Plasmodium falciparum Eukaryota; Alveolata;
                                                                                                                                                                                                                                                                                        01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
                                                                                                                                                                                                                                                                                                                        O77375 PRELIMINARY;
O77375;
O1-NOV-1998 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spiegel L.A., Huang E.N., Nascimento L.U., de la Bastide M., Vil D.M., Preston R.R., Matero A., Shah R., O'Shaughnessy A., Rodriguez M., Shekher M., Schutz K., See L.H., Swaby I., Habermann K., Dedhia N.N., Mewes H.W., Lemcke K., Mayer K.F.X.;
                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                          DNA-directed RNA polymerase PFC0805W, MAL3P6.20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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"Arabidopsis thaliana
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falciparum
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complete nucleotide sequence
iparum .";
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llarity 100.0%;
Conservative C
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                                                                                                                                            PubMed=10448855;
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Apicomplexa;
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ienssen R.,
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Pred. No. 2.4e+02;
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56E59466A597F63D CRC64;
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               of chromosome
                                                                                                                                                                                                                        Haemosporida; Plasmodium.
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Parnell L.D.,
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             Flasmodium
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                                                                                       OBTTC2; PRELIMINARY;
OBTTC2;
01-JUN-2002 (TIEMBLIE1. 2
01-JUN-2002 (TIEMBLIE1. 2
01-JUN-2002 (TIEMBLIE1. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q985W5
Q985W5;
Q1-OCT-2001
Q1-OCT-2001
Q1-MAR-2002
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InterPro; IPR000722; RNA_pol_A.
InterPro; IPR002879; RNA_pol_A2.
Pfam; PF006.33; RNA_pol_A; 1.
Pfam; PF01854; RNA_pol_A2; 1.
PROSITE; PS00115; RNA_POL_II_REPEAT; UNKNOWN_10.
                                                                                                                                                                                                                                                                                            Hypothetical SEQUENCE 1:
                                                                    Predicted protein. MA0515.
                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                               Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasan Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto Takeuchi C., Yamada M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein mlr7498. MLR7498.
SEQUENCE FROM N.A.
                                 Archaea; Euryarchaeota; Methanosarcinaceae; Metl
                                                        Methanosarcina acetivorans
                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-MAFF303099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhizobium loti (Mesorhizobium loti).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA-directed RNA polymerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 400:532-538(1999).
EMBL; Z98551; CAB11131.1;
                                                                                                                                                                                                                                                                                                                                 DNA Res.
                                                                                                                                                                                                                                                                                                                                          Mesorhizobium loti."
                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21082930; PubMed=11214968;
                                                                                                                                                                                                                                                                                                                                                        "Complete genome structure of
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                                                                                                                                                                                                                                                                                            ll protein; Complete 133 AA; 14309 MW;
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83.3%;
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Pred. No.
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Pred. No.
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E2C038E77A39DDED CRC64;
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                                                                                                                                                                                                                                                                                                                                                      nitrogen-fixing symbiotic bacterium
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                                                                                                                                         290
                                             Methanosarcinales;
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AB Bussey H., Storms R.K., Ahmed A., Bladcock K., Benes V., Botstein D.,

AA Araujo R., Aparicio A., Barrell B., Badcock K., Benes V., Botstein D.,

AA Araujo R., Aparicio A., Barrell B., Badcock K., Benes V., Botstein D.,

AA Araujo R., Aparicio A., Barrell B., Badcock K., Benes V., Botstein D.,

AA Araujo R., Aparicio A., Barrell B., Badcock K., Benes V., Botstein D.,

AA Downan S., Bruckner M., Carpenter J., Cherry J.M., Chung E.,

Churcher C., Coster F., Davis K., Davis R.W., Dietrich F.S.,

Delius H., Diraolo T., Dubois E., Dusterboft A., Duncan M., Floeth M.,

Fortin N., Friesen J.D., Fritz C., Goffeau A., Hall J., Hebling U.,

AA Heumann K., Hilbert H., Hillier L., Hunicke-Smith S., Hyman R.,

Johnston M., Kalman S., Kleine K., Komp C., Kurdi O., Lashkari D.,

AA Lew H., Lin A., Lin D., Louis E.J., Marathe R., Messenguy F.,

AA Mewes H.W., Mirtipati S., Moestl D., Muller-Auer S., Namath A.,

AA Nentwich U., Oefner P., Pearson D., Petel F.X., Pohl T.M.,

Purnelle D., Schafer M., Scharfen M., Scherens B., Schramm S.,

AA Vierendeels F., Vissers S., Voss H., Walsh S.V., Wambutt R., Wang Y.,

Wedler E., Wedler H., Winnett E., Zhong W.W., Zollner A., Vo D.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RX MEDLINE=21929760; PubMed=11932238;

RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

RA FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,

RA Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,

RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,

RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,

RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,

RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,

RA Linton L., McEwan P., McKernan D.E., Grahame D.A., Guss A.M.,

RA Linton L., McEwan P., McKernan D.E., Grahame D.A., Guss A.M.,

RA Linton L., McEwan P., McKernan D.E., Grahame D.A., Guss A.M.,

RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,

RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,

RA Ferry J.G., Jarrell K.F., Jing H., Mcaraio A.J.L., Paulsen I.,

RA Ferry J.G., Jarrell K.F., Jing H., Mcaraio A.J.L., Paulsen I.,

RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,

RA Mctcalf W.W., Birren B.;

RT "The genome of Methanosarcina acetivorans reveals extensive metabolic

RT and physiological diversity.";

RG Genome Res. 12:532-542(2002).

REMBL: ABBL: AAM03959.1; -.
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                                          Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z., Favello A., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
Johnston L.,
                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                     Submitted
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                      Nature 387:0-0(0).
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01-NOV-1996
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5; Conserv
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                     Langston
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83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                      of Saccharomyces cerevisiae
                     Latreille P.,
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Pred. No.
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1.5e+02;
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                     Menezes S.,
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RESULT 11
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Q98K16;
Q98K16;
01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel 20, Last annotation update)
                                                                                                                                                                                                                         Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto Matanabe A., Idesawa K., Ishikawa A., Kawashima K., Khnura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the nitrogen-fixing symbiotic bac Mesorhizoblum loti."; DNA Res. 7:331-338(2000).
                                                                                                                                                                                                     Complete
                                                                                                                                                                                                                                                                                                                                                STRAIN=MAFF303099;
                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Phyllobacteriaceae; Mesorhizobium.
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Submitted (SEP-1997)
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Taich A., Trevaskis E., Vignati D., Wilcox L., Wohldman
                                                                                                                                                                                                                                                                                                                                    MEDLINE=21082930; PubMed=11214968;
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IPRO00734; Lipase.
; IPRO00379; Ser_estrs_site.
; IPRO0120; LIPASE_SER; UNKNOWN_1.
PS00120; LIPASE_SER; UNKNOWN_1.
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83.3%;
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Pred. No. 1.7e+02;
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Pred. No.
                                                                                                                                                                                         934FF80EDAA9C8C4 CRC64;
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lman P., Va
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(TrEMBLrel.

15, 15,

Created) Last sequ

sequence update)

Q9KZH9

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Q936U1;
01-DEC-2001
01-DEC-2001
01-MAR-2002
 005611;
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STRAIN-LS46-6; TRANSPOSON-TN5046;
MEDLINE-21604134; PubMed-11763242;
Mindlin S.Z., Kholodii G.Y., Gorlenko Z.M., Minakhina S.V.
Minakhin L.S., Kalyaeva E.S., Kopteva A.V., Petrova M.A.,
Yurieva O.V., Nikiforov V.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Seeger T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J., Hongord T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL; AL353863; CAB88950.1;
                                                                                                                                                                                                                             Res. Microbiol. 152:811
EMBL; Y18360; CAC80080.
                                                                                                                                                                                                                                                        " Mercury resistance transposons of Gram-negative environmental
bacteria and their classification.";
                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria.
NCBI_TaxID=306;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical Pseudomonas s
                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                 Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmid pKLH466
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Bentley S.D., Chater K.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
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138 AA; 1
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(TrEMBLrel. 20, Last annotation update)
l 15.1 kDa protein.
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83.3%;
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Pred. No. 1.
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RESULT 14
Q9KCU0
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01-OCT-2000
01-MAR-2002
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STRAIN-KHP41; TRANSPOSON=TN5041;
MEDLINE=97419493; PubMed=9274008;
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01-JUL-1997 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
Transposon Tn5041 DNA.
                                                                                         Pfam; PF02517; Abi; 1.
Hypothetical protein; Complete
SEQUENCE 200 AA; 22915 MW;
                                                                                                                                                          EMBL; AP001512; BAB05198.1; -. InterPro; IPR003675; Abi.
                                                                                                                                                                                                   "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilia Nucleic Acids Res. 28:4317-4331(2000).
                                                                                                                                                                                                                                                                                      STRAIN-C-125 / JCM 9153;
MEDLINE-20512582; PubMed-11058132;
Takani H., Nakasone K., Takaki Y., Maeno G., S:
Fuji F., Hirama C., Nakamura Y., Ogasawara N.,
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=C-125 / JCM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Host-dependent transposition of Tn5041."; Russ. J. Genet. 36:365-373(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nikiforov V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas sp.
Bacteria; Proteobacteria.
                                                                                                                                                                                                                                                                      Horikoshi K.;
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      Conservative
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                       94.1%;
83.3%;
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83.38;
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., Kuhara S
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                                                                                       CRC64;
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RESULT 15
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AC Q9RKX
DT 01-MA
DT 01-MA
DT 01-MA
DT 01-MC
GN SCO14
OS Strep
OC Bactee
OC Actin
RN [1]
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Search completed: January 3, 2003, 15:31:56 Job time: 22.3182 secs
                                                                                                                                                      Query Match 94.1
Best Local Similarity 83.3
Matches 5; Conservative
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STRAIN-A3(2) / M145;

Bentley S.D. Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

Bentley S.D., Chater K.F., Larris D.E., Quail M.A., Kleser H.,

Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,

Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,

Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neil S.,

Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,

Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,

Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                               "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2)."
Nature 417:141-147(2002).
EMBL; AL133213; CAB61673.1; -
SEQUENCE 230 AA; 23916 MW; 5E87093F7CC1CC26 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces coelicolor.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID-1902;
[1]
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative integral membrane protein.
sccol418 OR SC6D7.21C.
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83.3%; Pred. No. 1.9e+02;
tive 1; Mismatches 0; Indels
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Database :
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Maximum DB seq
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1 LLIWIP 6
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/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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US-08-995-659-16
US-09-215-649A-16
US-09-215-649A-16
US-09-215-649A-16
US-09-27-780-16
US-08-518-835-5
US-08-474-040-21
US-08-487-278-21
US-08-487-200-21
US-08-484-537-21
US-08-484-537-21
US-08-484-537-21
US-08-484-537-21
US-08-474-040-67
US-08-477-728-67
US-08-474-040-67
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US-08-436-717-23
US-08-621-751A-14
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24	24	19	19	19	354	270	240	219	146	133	132	132	132	131	131	131	131
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US-08-162-102C-47	US-08-162-102C-27	US-08-976-288A-66	US-08-129-930B-66	us-07-977-696C-66	US-09-393-627B-28	US-09-532-856-7	US-09-301-593-36	US-08-902-516-2	US-08-653-402B-12	PCT-US93-11611-9	US-08-483-632-2	US-08-483-636-2	US-08-379-057-16	US-08-579-378A-18	US-08-579-378A-14	US-08-484-537-67	US-08-836-561-25
Sequence 47, Appl	Sequence 27, Appl	Sequence 66, Appl	Sequence 66, Appl	Sequence 66, Appl	•	Sequence 7, Appli	Sequence 36, Appl	Sequence 2, Appli	Sequence 12, Appl	Sequence 9, Appli	Sequence 2, Appli	Sequence 2, Appli	•	Sequence 18, Appl	Sequence 14, Appl	•	Sequence 25, Appl

ALIGNMENTS

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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-996-139-16
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                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA:
APPLICATION UNBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
PRIOR APPLICATION DATA:
APPLICATION UNBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNET/AGENT INFORMATION:
                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.
SOFTWARE: Microsoft Word for Power Macintosh
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                    SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acids
                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                        NAME: Perkins, Patricia Anne REGISTRATION NUMBER: 34,693 REFERENCE/DOCKET NUMBER: 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 51 Uni
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                                                          amino acid
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                                                                                         20 amino acids
                                                                                                                                                        (206)233-0644
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22 DECEMBER 1997
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; MOLECULE TYPE:
US-08-995-659-16
RESULT 3
US-09-215-649A-16
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                                                                                                                         Matches
                                                                                                                                     Query Match
Best Local Similarity
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Best Local S
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INFORMATION FOR SEQ ID NO:
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APPLICANT:
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APPLICATION NUMBER
                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 34,693
REFERENCE/FOCKET NUMBER: 35
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia
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APPLICATION NUMBER: US
FILING DATE: 07 MARCH
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TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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                                                                11 LLLWVP 16
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                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: USSN 08/772,330 FILING DATE: 23 DECEMBER 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
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                                                                                                                                                                                            protein
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14 OCTOBER 1997
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22 DECEMBER 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
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CH 1997
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Pred. No.
                                                                                                                                     Score 31; DB Pred. No. 21;
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Macintosh 6.0.1
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US-09-320-424-25
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Best Local S
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
EARLIER APPLICATION NUMBER: 09/048,641
EARLIER FILING DATE: 1998-03-26
EARLIER APPLICATION NUMBER: 08/670,354
                                                               CURRENT APPLICATION NUMBER: US/09/320,424
CURRENT FILING DATE: 1999-05-26
EARLIER APPLICATION NUMBER: 09/190,046
EARLIER FILING DATE: 1998-11-10
                                                                                                                                                         APPLICANT: Wiley, Steven R.
APPLICANT: Goodwin, Raymond G.
TITLE OF INVENTION: Cytokine that Induces Apoptosis
FILE REFERENCE: 2835-E
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nes 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/215,649A
FILING DATE: 17-Dec-1998
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TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/996,139
FILING DATE: <UNKNOWN>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (206)233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 34,693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 20 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
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Pred. No.
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21;
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EARLIER APPLICATION NUMBER: 08/548,368
EARLIER FILING DATE: 1995-11-01
EEARLIER APPLICATION NUMBER: 08/496,632
EARLIER FILING DATE: 1995-06-29
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 25
LENGTH: 20
                                                                                 TOPOLOGY: linear;
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ
US-09-577-780-16
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Whiches 4; Conserve
Query Match
Best Local Similarity
4; Conserv
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GENERAL INFORMATION:
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                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 16:
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                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: PERKINS, PAITICIA Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/577,780
FILING DATE: 24-May-2000
CLASSIFICATION: <UNknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
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                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/995,659
FILING DATE: CUNKNOWN>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6
                                                                                                                                                                                                                               TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: WA
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                                                                                                                                                             TYPE: amino acid
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                  2;
                Score 31; DB 4;
Pred. No. 21;
2; Mismatches
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                                                                                                                                                                                                                                        RESULT 7
US-07-634-278-21
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                                                                                                                                                                                                   Sequence 21, Appli
Patent No. 5530101
                                                                                                                                                                                                                                                                                                                                                                                          Best
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                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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APPLICANT: CHESTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: DIGICLIO, FRANK S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 1109
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
                                                                                                                                    APPLICANT: QUEEN, Cary L. APPLICANT: CO, Man Sung APPLICANT: SCHNEIDER, Wil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: HOEFFLER, JAMES P. TITLE OF INVENTION: NOVEL SYS
                                   CORRESPONDENCE ADDRESS:
                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                  APPLICANT: SELICK, Harold E. TITLE OF INVENTION: IMPROVE
                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/518,835 FILING DATE: 24-AUG-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                           11 LLLWVP 16
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STATE: NEW YORK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                         1 LLIWIP 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1: 21 amino acids amino acid
                                                                                                                                                                                                                        Application US/07634278
                                                                                                  CO, Man Sung
SCHNEIDER, William P.
LANDOLFI, Nicholas F.
COELINGH, Kathleen L.
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379 Lytton Avenue
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                   Townsend and Townsend Khourie and Crew
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) 742-4366
) NO: 5:
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                                                                  IMPROVED HUMANIZED IMMUNOGLOBLINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOVEL SYSTEM FOR ISOLATING AND IDENTIFYING EUKARYOTIC CELLS TRANSFECTED WITH GENES AND VECTORS, HOST CELLS AND METHODS THEREOF
                                                    113
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Pred. No.
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22;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COUNTRY:

California

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-634-278-21
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Best Local Similarity
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APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-477-728-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           equence 21,
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INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tent No.
                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                       APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUN
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
                               APPLICATION NUMBER: US/08/477,728 FILING DATE: 07-JUN-1995 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                           ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: Palo Alto
                                                                                                                                                                                                                    COUNTRY: US C
ZIP: 94111
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5585089
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66.7%;
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Pred. No. 1.2e+02;
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-477-728-21
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Patent No.
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Best Local
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            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/
FILING DATE: 13-FEB-1989
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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LENGTH: 126 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,;
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/310,252 FILING DATE: 13-FEB-1989 PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
FILING DATE: 28-SEP-
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                    APPLICATION NUMBER: US/08/474,040 FILING DATE: 07-JUN-1995 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                               COUNTRY: UZIP: 94301
                                                                                                                                                                                                                                                                                                                                                CITY: Palo Alto
STATE: California
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5. 5693761
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COELINGH, Wicholas F.
COELINGH, Kathleen L.
SELICK, Harold E.
NVENTION:
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SCHNEIDER, William
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28-DEC-1988
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                                                                                                                   US 07/634,278
                                                                                   us 07/590,274
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pred. No. 1.2e+02;
2; Mismatches 0;
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US-08-487-200-21
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APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
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TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
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REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELECOMMUNICATION INFORMATION:
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CITY: Palo Alto
STATE: Californ
                                                                                                                                                                                                   APPLICATION NUMBER: US 0' FILING DATE: 28-SEP-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LLIWIP 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/08487200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UMBER: US 07/290,975
28-DEC-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91.2%;
66.7%;
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Pred. No. 1
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                                                                                                                                          ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-656-586-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-487-200-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-656-586-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/08656586 Patent No. 5834597 GENERAL INFORMATION:
                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                 TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joseph O.
REGISTRATION NUMBER: 37.505
REFERENCE/DOCKET NUMBER: 1182:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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STREET: Two LILLS
STATE: San Francisco
STATE: California
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APPLICANT: Cole, Michael S.
APPLICANT: Cole, Michael S.
APPLICANT: Anasetti, Claudio
TITLE OF INVENTION: Mutated No. 5834597activating IgG2 Domains and
TITLE OF INVENTION: Anti-CD3 Antibodies Incorporating the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1
11 LLLWVP 16
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/0 FILING DATE: 31-MAY-1996
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                                                                                                                                                                                                TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
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                                   1 LLIWIP 6
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                                                                                                                                                                                            amino acid
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                                                                       Conservative
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                                                                                      91.2%;
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66.7%;
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                                                                   Score 31; DB 2;
Pred. No. 1.2e+02;
2; Mismatches (
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Pred. No. 1.2e+02;
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                                                                                                     Length 126;
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                                                                     Indels
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                                                                   Gaps
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RESULT 12 US-08-484-537-21 ; Sequence 21, Application US/08484537 ; Patent No. 6180370

GENERAL INFORMATION:

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RESULT 13
US-08-649-100-33
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                                                                                                                                                  Patent No. 6114507 GENERAL INFORMATION:
                                                                                                                                                                                          Sequence 33,
                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE (2007)
                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: protein 08-484-537-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO:
           APPLICANT: NAGATA, SHIGEKAZU
APPLICANT: CO, MAN SUNG
APPLICANT: CO, MAN SUNG
APPLICANT: VASQUEZ, MAXIMILIANO
TITLE OF INVENTION: ANTI-FAS LIGAND ANTIBODY AND ASSAY
TITLE OF INVENTION: METHOD USING THE ANTI-FAS LIGAND ANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
                                                                     APPLICANT: SHIRAKAWA, KAMON
APPLICANT: MATUSUE, TOMOKAZU
APPLICANT: NAGATA, SHIGEKAZU
APPLICANT: CO, MAN SUNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING LALL CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
APPLICATION NUMBER: US/07/634,278
APPLICATION NUMBER: US/07/634,278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: STREET: STREET: Palo Alto CITY: Palo Alto CTATE: California
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TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
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NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/484,537 FILING DATE:
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                                                                                                                                                                      3, Application US/08649100 6114507
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CO, Man Sung
SCHNEIDER, William
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                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                   91.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                     Length 126;
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RESULT 14
US-08-348-548-6
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TOPOLOGY: linear;
MOLECULE TYPE: peptide
US-08-649-100-33
                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 023001
Patent No. 023001
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Berdoz,
APPLICANT: Kraehenbuhl, Jean Pierre
APPLICANT: Kraehenbuhl, Jean Pierre
APPLICANT: Kraehenbuhl, Jean Pierre
APPLICANT: VARIABLE REGIONS OF IMMUNOGLOBULIN GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/08348548 Patent No. 6258529
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Best Local :
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APPLICATION NUMBER: US/08/348,548
FILING DATE: 01-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06132/0090
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street, Suite 3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                               STREET:
CITY: B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/649,100 FILING DATE: CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: PO BOX 747 CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                            STATE: MA
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ZIP: 22040-0747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
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                                         06132/009001
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APPLICANT: Vasquez, Maximiliano
APPLICANT: Landolfi, Nicholas F.
APPLICANT: Tsurushita, Naoya
APPLICANT: Queen, Cary L.
APPLICANT: Queen, Cary L.
APPLICANT: Protein Design Labs, Inc.
TITLE OF INVENTION: Humanized Antibodies To Gamma-Interferon
FILE REFERENCE: 011823-008110US
CURRENT APPLICATION NUMBER: US/09/450,520A
CURRENT FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: 60/110,523
PRIOR FILING DATE: 1998-12-01
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 128
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:human-mouse
OTHER INFORMATION: transgenic construct HuZAF VL
US-09-450-520A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: '128 amino acids
TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-348-548-6
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Search completed: January 3, 2003, 15:34:27 Job time: 10 secs
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Best Local Similarity 66.7%;
Matches 4; Conservative
                                                                                                                                                                  Query Match 91.2%;
Best Local Similarity 66.7%;
atches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OU-7 15
09-450-520A-6
Sequence 6, Application US/09450520A
Patent No. 6329511
                                                                                     11 LLLWVP 16
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                                                                                                           1 LLIWIP 6
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                                                                                                                                                                  Score 31; DB 4; Length 128; Pred. No. 1.2e+02; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 31; DB 4; Length 128; Pred. No. 1.2e+02; 2; Mismatches . 0; Indels
                                                                                                                                                                     0;
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Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 number
                                                                                                                                                                                                                                                                                                                                                                                                              DB seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                              length: 0
length: 2000000000
          US-09-543-188A-3
34
1 LLIWIP 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117078 seqs, 18951520 residues
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                                                                                                                                                                                                                                                                                                                               Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                             Published_Applications_AA: *
/cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenCore version (c) 1993 - 2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (without alignments)
23.825 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

18 19	17	16	15	14	13	12	11	10	9	8	7	o	ഗ	4	ω	2	1	Result No. S
<u>υ</u> ω	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	32	34	Score
91.2	91.2	91.2	91.2	91.2	91.2	91.2	91.2	91.2	91.2	91.2	91.2	91.2	91.2	91.2	91.2	94.1	100.0	Query Match
147	144	134	132	131	130	128	128	123	107	107	106	98	80	20	20	177	87	Query Match Length
10	10	10	9	10	10	10	10	10	10	10	10	10	10	10	9	10	10	DB
US-09-894-018-131	US-09-894-018-129	US-09-881-823-2	US-09-879-461-2	US-09-286-240-2	US-09-894-018-99	US-09-992-524-6	US-09-881-823-14	US-09-894-018-109	US-09-894-018-103	US-09-894-018-93	US-09-894-018-95	US-09-894-018-101	US-09-894-018-97	US-09-871-856-16	US-09-877-650-16	US-09-764-864-942	US-09-864-761-40310	ID
Sequence 131, App	Sequence 129, App	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 99, Appl	6, 2	Sequence 14, Appl	Sequence 109, App	Sequence 103, App	Sequence 93, Appl	Sequence 95, Appl	Sequence 101, App	Sequence 97, Appl	Sequence 16, Appl	Sequence 16, Appl	Sequence 942, App	Sequence 40310, A	Description

## ALIGNMENTS

RESULT 1 US-09-864-761-40310

GENERAL INFORMATION:

Sequence 40310, Application US/09864761 Patent No. US20020048763A1

```
APPLICANT: Penn, Sharron G.
APPLICANT: Hancel, David K.
APPLICANT: Hancel, David K.
APPLICANT: Hancel, David K.
APPLICANT: Hancel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENITION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica xl
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-02-04
PRIOR PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: CT/US01/0066
PRIOR APPLICATION NUMBER: CT/US01/0066
PRIOR APPLICATION NUMBER: CT/US01/0066
PRIOR APPLICATION NUMBER: CT/US01/0066
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: CT/US01/00669
PRIOR APPLICA
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RESULT 3
US-09-877-650-16
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Best Local Similarity
Conserva
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-864-942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-764-864-942
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Best Local Similarity
6; Conserva
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                                                                                        Sequence 16, Application US/09877650 Patent No. US20020169117A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 942, Application US/09764864 Patent No. US20020132753A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEO ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEO ID NO 40310
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OTHER INFORMATION: E
OTHER INFORMATION: E
OTHER INFORMATION: E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/764,864 CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prior application data removed - consult PALM or NUMBER OF SEQ ID NOS: 1792
OFTWARE: PatentIn Ver. 2.0
Q ID NO 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 87
TYPE: PRT
ORGANISM: Homo sapiens
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OTHER INFORMATION:
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                                                                                                                                                                                                                                        35 LLLWIP 40
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                                                                                                                                                                                                                                                                              1 LLIWIP 6
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APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30 APPLICATION NUMBER: US 60/234,687 FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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NN: EXPRESSED IN LUNG, SIGNAL = 1.5

NN: EXPRESSED IN PLACENTA, SIGNAL = 1.3

NN: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1

NN: EXPRESSED IN BONE MARROW, SIGNAL = 1.1

NN: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5

NN: EXPRESSED IN HEART, SIGNAL = 1.2

NN: EXPRESSED IN HEART, SIGNAL = 1.2

NN: EXPRESSED IN BRAIN, SIGNAL = 1.3

NN: EXPRESSED IN BRAIN, SIGNAL = 1.3
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                            Length 177;
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                                                                                                                                                                                                                                                                                                                                                                                     Sequence 16, Application US/09871856 Patent No. US20020081720A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local 9
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nes 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/877,650
FILING DATE: 08-Jun-2001
CLASSIFICATION: CUNknown>
                 COMPUTER: Apple Power Macintosh OPERATING SYSTEM: Apple Operating System 7. SOFTWARE: Microsoft Word for Power Macintos CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/995,659
EILING DATE: 1997-12-22
APPLICATION NUMBER: USSN 08/813,509
EILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                   Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Anderson, Dirk M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patrici
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                   CITY: Seattle
STATE: WA
                                                                                                                                                                                                                         ADDRESSEE: Immunex Corporati
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Perkins, Patricia Anne REGISTRATION NUMBER: 34,693
                                                                                                                                          ZIP: 98101
                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
APPLICATION NUMBER: US/09/871,856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                             Galibert, Laurent
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                                                                                                                                                                                                                                             Immunex Corporation,
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Pred. No. 13;
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                                                                                                                                                                                                                                               Law Department
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                                        Macintosh
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/996,139

FILING DATE: 31-May-2001 CLASSIFICATION: <Unknown>

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APPLICANT: Newman, Mark
APPLICANT: Brown, David
TITLE OF INVENTION: METODS AND SYSTEM FOR OPTIMIZING
TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY
FILE REFERENCE: 39963-20033.00
CURRENT APPLICATION NUMBER: US/09/894,018
CURRENT FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: PCT/US00/35568
PRIOR APPLICATION NUMBER: US 60/173,390
PRIOR FILING DATE: 1999-12-28
PRIOR FILING DATE: 1999-12-28
PRIOR FILING DATE: 1999-12-28
QΥ
                                                                                                      ; OTHER INFORMATION: HCV.3s2(-3) US-09-894-018-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-894-018-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
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                                                                                                                                                                                       PRIOR FILING DATE: 2001-04-16
NUMBER OF SEQ ID NOS: 368
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 97
LENGTH: 80
                                  Matches
                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 97, Application US/09894018 Patent No. US20020119127A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: EPIMMUNE, Inc. APPLICANT: Sette, Alessa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                         FEATURE:
                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (206)587-0430
TELEPAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
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1 LLIWIP 6
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NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 16:
                                  4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: USSN 08/772,330 FILING DATE: 23 DECEMBER 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 20 amino acids
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                                  Conservative
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66.7%;
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66.7%;
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Pred. No. 1
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                                                 Score 31;
Pred. No.
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                                  Mismatches
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                                               46;
                                                                   DB 10;
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                                                                  Length 80;
                                 Indels
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                               Gaps
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TITLE OF INVENTION: METODS AND SYSTEM FOR OPTIMIZING TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY FILE REFERENCE: 39963-20033.00

CURRENT APPLICATION NUMBER: US/09/894,018

CURRENT FILING DATE: 2001-06-27

PRIOR APPLICATION NUMBER: PCT/US00/35568

PRIOR FILING DATE: 2000-12-28

PRIOR APPLICATION NUMBER: US 60/173,390

PRIOR FILING DATE: 1999-12-28

PRIOR FILING DATE: 1999-12-28

PRIOR FILING DATE: 1990-13-28

PRIOR FILING DATE: 3001-04-16

NUMBER OF SEQ ID NOS: 368

SOFTMARE: FastSEQ for Windows Version 4.0

SEQ ID NO 95

LENOTH: 106
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CURRENT APPLICATION NUMBER: US/09/894,018

CURRENT FILING DATE: 2001-06-27

PRIOR APPLICATION NUMBER: PCT/US00/35568

PRIOR FILING DATE: 2000-12-28

PRIOR APPLICATION NUMBER: US 60/173,390

PRIOR APPLICATION NUMBER: US 60/284,221

PRIOR FILING DATE: 1999-12-28

PRIOR APPLICATION NUMBER: US 60/284,221

PRIOR FILING DATE: 2001-04-16
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 101
LENGTH: 98
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APPLICANT:
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APPLICANT: Sette, Alessa
APPLICANT: Chestnut, Rob
APPLICANT: Livingston, B
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: EPIMMUNE, Inc.
APPLICANT: Sette, Alessandro
APPLICANT: Chestnut, Robert
APPLICANT: Livingston, Brian
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Newman, Mark
Brown, David
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Livingston, Brian
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Brown, David
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66.7%;
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TITLE OF INVENTION: METODS AND SYSTEM FOR OPTIMIZING TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY FILE REFERENCE: 39963-20033.00

CURRENT APPLICATION NUMBER: US/09/894,018

CURRENT PILING DATE: 2001-06-27

PRIOR APPLICATION NUMBER: PCT/US00/35568

PRIOR FILING DATE: 2000-12-28

PRIOR FILING DATE: 1200-12-28

PRIOR APPLICATION NUMBER: US 60/173,390

PRIOR FILING DATE: 1999-12-28

PRIOR APPLICATION NUMBER: US 60/284,221

PRIOR FILING DATE: 2001-04-16

NUMBER OF SEQ ID NOS: 368

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 93

LENGTH: 107
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US-09-894-018-93
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US-09-894-018-95
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Best Local Similarity bo..
"""hes 4; Conservative
APPLICANT: LATER APPLICANT: Baker, Denisw APPLICANT: Baker, Denisw APPLICANT: Newman, Mark APPLICANT: Brown, David TITLE OF INVENTION: METODS AND SYSTEM FOR OPTIMIZING TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY FILE REFERENCE: 39963-20033.00 CURRENT APPLICATION NUMBER: US/09/894,018 CURRENT FILING DATE: 2001-06-27
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                                                                                                                                                                                                                                                      Sequence 103, Application US/09894018 Patent No. US20020119127A1
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APPLICANT: Sette, Alessa
APPLICANT: Chestnut, Rob
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Newman, Mark
Brown, David
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Chestnut, Robert
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Pred. No. 59;
2; Mismatches
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Pred. No.
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RESULT 11

US-09-881-823-14

; Sequence 14, Application US/09881823

; Patent No. US20020068066A1

; GENERAL INFORMATION:
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APPLICANT: Brown, David
TITLE OF INVENTION: METODS AND SYSTEM FOR OPTIMIZING
TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY
FILE REFERENCE: 39963-20033.00
CURRENT APPLICATION NUMBER: US/09/894,018
CURRENT FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: PCT/US00/35568
PRIOR FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: US 60/173,390
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: US 60/284,221
PRIOR APPLICATION NUMBER: US 60/284,221
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US-09-894-018-103
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Matches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 109
LENGTH: 123
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Matches
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SOFTWARE: FRACTSEQ for Windows Version 4.0
SEQ ID NO 103
LENGTH: 107
TYPE: PRT
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                                                                                                                                                                                                                                         Query Match
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APPLICANT: Sette, Alessandr
APPLICANT: Chestnut, Robert
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                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2001-04-16
                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                   FEATURE:
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Newman, Mark
Brown, David
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66.7%;
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Pred. No.
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Pred. No.
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67;
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59;
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Baker, Denisw

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RESULT 13
US-09-894-018-99
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; OTHER INFORMATION:
; OTHER INFORMATION:
US-09-992-524-6
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; TYPE: PRT
; ORGANISM: Murine
US-09-881-823-14
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Conserve
                                                                GENERAL INFORMATION:
                                                                                Sequence 99, Application US/09894018 Patent No. US20020119127A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/881,823
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 07/378,577
PRIOR FILING DATE: 1999-08-20
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.0
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/09992524 Patent No. US20020091240A1
                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Queen, Cary L.

APPLICANT: Protein Design Labs, Inc.
TITLE OF INVENTION: Humanized Antibodies To Gamma-Interferon
FILE REFERENCE: 011823-00811005
              APPLICANT: EPIMMUNE, Inc.
APPLICANT: Sette, Alessa
APPLICANT: Chestnut, Rob
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 13 SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/992,524
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: 09/450,520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1999-11-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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APPLICANT: CHEN, LI
TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries
FILE REFERENCE: 22851-032
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 128
TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                       4; Conservative
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            Sette, Alessandro
Chestnut, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANDERSON, MAXWELL MORRISON, SHERIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                        Description of Artificial Sequence:human-mouse transgenic construct HuZAF VL
                                                                                                                                                                                                                                                                       91.2%;
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66.7%;
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69;
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APPLICANT: Newman, Mark

APPLICANT: Brown, David

TITLE OF INVENTION: METODS AND SYSTEM FOR OPTIMIZING

TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY

FILE REFERENCE: 39963-20033.00

CURRENT APPLICATION UMBER: US/09/894,018

CURRENT FILING DATE: 2001-06-27

PRIOR APPLICATION NUMBER: PCT/US00/35568

PRIOR APPLICATION NUMBER: US 60/173,390

PRIOR FILING DATE: 2001-02-28

PRIOR APPLICATION NUMBER: US 60/173,390

PRIOR FILING DATE: 1999-12-28

PRIOR FILING DATE: 2001-04-16

PRIOR FILING DATE: 2001-04-16

PRIOR FILING DATE: 2001-04-16

NUMBER: OS 60/284,221

PRIOR FILING DATE: 2001-04-16
                                                                                                                                                                                                                RESULT 15
US-09-879-461-2
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US-09-286-240-2
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Best Local Similarity
""" (Conserve
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; OTHER INFORMATION: HCV.3s3
US-09-894-018-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-286-240-2
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SEQ ID NO 99
LENGTH: 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Fett, James W
TITLE OF INVENTION: Chimeric and Humanized Antibodies to Angiogenin
FILE REFERENCE: 10498/74073
                                                                                                                                                                          Sequence 2, Application US/09879461 Publication No. US20020193575A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 2
LENGTH: 131
TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09286240 Patent No. US20020010320A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/286,240
CURRENT FILING DATE: 1999-04-05
NUMBER OF SEQ ID NOS: 25
                                                                                                           GENERAL INFORMATION:

APPLICANT: Holmes, Stephen D.

Gross, Mitchell S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
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                                                                            TITLE OF INVENTION:
                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                          4;
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                                                                                               Sylvester, Daniel R.
SmithKline Beecham Corporation
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66.7%;
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                                                        Recombinant IL4 / Treatment of IL4
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Pred. No.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                        IL4 Antibodies Useful in f IL4 Mediated Disorders
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70;
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STREET: Corporate Intellectual Property, UW2220 - 709

Swedeland Rd.

CITY: King of Prussia
STATE: PA

COUNTRY: USA

ZOUNTRY: USA

COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

COUNTRY: LIMP OF PRICE PROPERTY

MEDIUM TYPE: Floppy disk

COPERATING SYSTEM: PC-DOS_WS-DOS

SOFTWARE: PACENTEM: PC-DOS_WS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/879,461

FILING DATE: (JN-000)

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Search completed: January 3, 2003, 15:52:04 Job time : 4.77273 secs
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Minimum DB
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          3883888
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Gapop 10.0 , Gapext 0.5
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        Query
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**(SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:*

**(SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*

**(SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*

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**(SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:*

**(SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*

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Listing first 45 summaries
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        137
137
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                              AAM41991
AAM40205
ABG30232
AAU32016
ABB67564
AAU000427
                                                                                                                                                                                       AAU11827
ABB89811
AAM96472
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Human polypeptide
Human polypeptide
Novel human diagno
Novel human secret
Drosophila melanog
Caenorhabditis ele
Caenorhabditis ele
                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                          Human
                                                                                                                                                                                                                Peptide ligand for Human polypeptide
                                                                                                                                                                                          reproductive
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Propionibacterium	AAU43406	22	160	77.3	34	45
Novel human diagno	ABG01550	22	130	77.3	34	44
Human EST encoded	AAM24385	22	103	77.3	34	43
onibact	AAU50181	22	76	77.3	34	42
Novel human diagno	ABG01631	22	62	77.3	34	41
2	ABB72639	23	17	77.3	34	40
IL-1 antagonist pe	AAB17743	21	17	77.3	34	39
×	AAY09966	20	17	77.3	34	38
IL-1RtI binding pe	AAW58320	19	17	77.3	34	37
	AAW68833	19	17	7.	34	36
Peptide containing	AAW16194	18	17	7.	34	ω 5
platelet gl	AAW32770	18	10	77.3	34	34
Novel human secret	AAU33181	22	533	9	<u>3</u> 5	ω ω
sseria meningi	AAY74306	21	524	9.	ω G	32
E. coli cellular p	AAU34459	22	475	9.	35	31
Human G-protein co	ABB76184	23	382	9.	35	30
Haemophilus influe	AAU35593	22	360	9	35	29
Novel human diagno	ABG10973	22	195	9.	35	28
`	AAM89871	22	117	9	35	27
Human signal pepti	AAY87271	21	109	9	35	26
peptide	ABG37801	23	83	9.	ယ် G	25
Human ORF623 prote	ABP31650	23	54	9.	35	24
Listeria monocytog	ABB47832	23	719	۲.	36	23
Propionibacterium	AAU46431	22	331	1.	36	22
Human type 3 inosi	AAR99850	17	2701	٠	37	21
	AAM93820	22	836	84.1	37	20
	AAW14440	18	561	84.1	37	19
	ABB49843	23	461	84.1	37	18
Streptococcus poly	ABP30101	23	458	84.1	37	17
Human NOV8 protein	AAU91293	23	415	84.1	37	16
есе	AAR14114	12	415	84.1	37	15
Group B Streptococ	AAU03712	22	393	84.1	37	14
_	076	22	385	84.1	37	13
Streptococcus poly	ω	23	384	84.1	37	12
Human secreted pro	AAU01575	22	27	84.1	37	11

## ALIGNMENTS

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RESULT 1
AAU11827
                                                                                                                                                                                                       Prion protein; Prp; ligand; octapeptide motif; scrapie; prion-associated disease; Creutzfeldt-Jakob disease; Gerstmann-Straussler-Scheinker disease; fatal familial insomnia; feline spongiform encephalopathy; bovine spongiform encephalopathy; transmissible mink encephalopathy; exotic ungulate encephalopathy;
        WPI; 2002-061944/08
                               Hammond DJ, Wiltshire VR, Carbonell R,
                                                   (VITE-) VI
                                                                            05-APR-2000; 2000US-0543188
                                                                                                                           18-OCT-2001.
                                                                                                                                                 WO200177687-A2.
                                                                                                                                                                        Synthetic
                                                                                                                                                                                               chronic wasting disease.
                                                                                                                                                                                                                                                                            Peptide ligand for Prion protein, PrP, #2.
                                                                                                                                                                                                                                                                                                      26-MAR-2002
                                                                                                                                                                                                                                                                                                                             AAU11827;
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                                                                                                  05-APR-2001; 2001WO-US11150
                                                     TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                     (first entry)
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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a ligand of less than 6 kD that binds to a polypeptide containing the sequence GlyTyrGlyGlnProHisGlyGly (A) or an analogue that is the retro-inverso isomer of (A). The sequence A is an octapeptide motif from the prion protein (PrP). The ligands are identified by binding assays with the peptide (A) or peptides containing (A). The ligands are used for detecting prion proteins (or prions) in biological or environmental samples, e.g. for diagnosis, also for removing them from samples, for treating or retarding development of prion-associated diseases, especially Creutzfeldt-Jakob diseases (in latrogenic, new variant, familial or sporadic forms), but also Gerstmann-Straussler-Scheinker disease, fatal familial insomnia, scrapie, bovine or feline spongiform encephalopathy, transmissible mink or exotic ungulate encephalopathy, or chronic wasting disease. The
                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiucer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder neurological disease; infection; human; secreted protein.
The invention relates to novel genes (ABL89449-ABL90853) and proteins
                                     Claim 11;
                                                                       disorders
                                                                                   Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative
                                                                                                                                                          N-PSDB;
                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                            19-MAY-2000; 2000US-205515P
                                                                                                                                                                                                                                                                                                                                                                                    WO200190304-A2
                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human polypeptide SEQ ID NO 2187.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB89811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB89811 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 16; Page 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New ligands for prion proteins, useful for detection or removal or prions and for treating prion-associated diseases, recognize a specific
                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                              18-MAY-2001; 2001WO-US16450
                                                                                                                                                                                                                                                                                                                                                29-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present sequence is a ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             octapeptide
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                                                                                                                                                         2002-122018/16
DB; ABL90220.
                                                                                                                                                                                                            CE,
                                     SEQ
                                                                                                                                                                                                           Rosen CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                 ID NO 2187; 2081pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
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                                                                                                                                                                                                                                           SCI INC
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Pred. No. 7.8e+05;
Pred. No. 7.8e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disorder;
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RESULT 3
AAM96472
ID AAM9
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Best Local
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30-JUN-2000;
07-JUL-2000;
                                               11-JUL-2000;
14-JUL-2000;
26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
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19-MAY-2000;
07-JUN-2000;
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16-MAR-2000;
17-MAR-2000;
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11-JUL-2000;
                                      14-AUG-2000;
                                                                                                                                                                                                                                                                                                                 17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                    cancer; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; reproductive system related antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 WLYWLP 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            reproductive system related antigen SEQ ID NO:
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5; Conserv
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                                                                                                   2000US-0215135.
2000US-0216647.
2000US-0216880.
2000US-0217487.
2000US-0217496.
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2000US-0180628.
2000US-0184664.
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                       2000US
2000US
2000US
2000US
2000US
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                                                                                                                                                                                                         2000US-0190076.
2000US-0198123.
                                                                                       2000US-0218290
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2000US-0189874
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s-0220964.
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Pred. No.
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13;
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2000US-0225267 2000US-0225268 2000US-0225270 2000US-0225277 2000US-0225757 2000US-0225757 2000US-0225759 2000US-0225759 2000US-0226681 2000US-0226681

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RESULT 4
AAM41991
ID AAM4
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                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 4; Conserv
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08-NOV-2000
08-NOV-2000
08-NOV-2000
08-NOV-2000
08-NOV-2000
08-NOV-2000
17-NOV-2000
17-NOV
                                                                                                                                                                                                                                                                                                     The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be us in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a protein of the invention.
                    AAM41991 standard; Protein;
                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; SEQ ID NO 5130; 1297pp +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-465570/50.
N-PSDB; AAL02442.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition % \left( 1\right) =\left\{ 1\right\} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rosen
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|14 WVYWVP 11
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2000US-0246610
2000US-0246611
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2000US-0249207
2000US-0249210
2000US-0249211
2000US-0249211
2000US-0249211
2000US-0249211
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2000US-0249216
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2000US-0249216
2000US-0249216
2000US-0249244
2000US-0249244
2000US-0249265
2000US-0249265
2000US-0249269
2000US-02503160
2000US-02503160
2000US-02503160
2000US-02511856
2000US-02511856
2000US-02511856
2000US-02511868
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2000US-0246527.
2000US-0246528.
2000US-0246532.
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                    235
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Pred. No. 22;
2; Mismatches
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                    AΑ
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence Listing; English.
                                                                                                                                                                                                       DB
22;
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be used
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18-AUG 2000
22-AUG 2000
22-AUG 2000
22-AUG 2000
23-AUG 2000
201-SEP 2000
01-SEP 2000
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02-SEP 2000
02-SE

2000US -0227182
2000US -0229287
2000US -0229287
2000US -0229343
2000US -0229343
2000US -0229513
2000US -0229513
2000US -0229513
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2000US -0232401
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2000US -0233688
2000US -0234274
2000US -0235883
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2000US -024647
2000US -0246478
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2000US -0246523
2000US -0246523

AAM41991;

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                                                       Query Match
Best Local
                                            Matches
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
13-AUG-2000;
14-SEP-2000;
19-OCT-2000;
                                                                                                                                          The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity. Parager Syndrome system suppression, Activinyinhibin activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                  Tang
Wang
Zhao
                                                                                        Sequence
                                                                                                               Note: The sequence specification.
                                                                                                                                                                                                                                                                                                        Example 2; SEQ ID NO 6922; 10078pp; English.
                                                                                                                                                                                                                                                                                                                             Novel nucleic acids and polypeptides, us such as central nervous system injuries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-DEC-2000; 2000WO-US34263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200153312-A1
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212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                leukaemia.
                      1 WLYWIP 6
                                                                                                                                     S disorders
AVMANA
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DB; AAI61147.
                                            4
                                                       Similarity
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Wang Z,
Zhou P,
                                                                                        235
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2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-062315.
2000US-0653450.
2000US-06393036.
2000US-0727344.
                                            Conservative
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Wehrman T, Xu C, Xue
Goodrich R, Drmanac
                                                                                                                         data
                                                      90.9%;
                                                                                                                         for
                                                                                                                                                                                                                                                                                                                                         polypeptides, useful for
                                           2;
                                                                                                                        this patent did
                                                      Score 40; DB Pred. No. 37;
                                          Mismatches
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Xue AJ,
nac RT;
                                                                 22;
                                                                                                                        not form part of the
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Yang Y,
                                                               Length 235;
                                                                                                                                                                                                                                                                                                                                         treating
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Zhang J;
                                                                                                                                                                                                                                                                                                                                          disorders
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CNS;
                                          Gaps
                                                                                                                        printed
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RESULT 5

밁 Q

Similarity

Conservative

0;

Indels

0,

Gaps

0,

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AAM40205
Query Match
Best Local S
Matches 4
                                                                                                                     The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as alzheimer's, parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, Drager Syndrome. System suppression, activity, activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JAN-2000;
25-APR-2000;
09-JUL-2000;
19-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang
Wang
                                                       Sequence
                                                                                  specification.
                                                                                                 Note: The sequence data
                                                                                                              C.N.S disorders.
                                                                                                                                                                                                                                                                                                                                              Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries - \!\!\!\!
                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-442253/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; heemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhao
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19-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chemokinetic;
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Wang Z,
Zhou P,
                                                         533
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2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
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2000US-0693036.
2000US-0727344.
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Wehrman T, X
Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
               90.98;
                                                                                                                                                                                                                                                                                                                   3350; 10078pp; English
                                                                                              for this patent did not form part of the printed
Score 40; DB Pred. No. 84; 2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen R, Ma Y, Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Drmanac RT;
                            22;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Qian XB,
Yang Y,
                           Length 533;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Ren F, V
Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang D;
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RESULT 6
ABG30232
Вр
                              δÃ
                                                                                                                                              PX PX OX XXX X DX XXX
                                                                    Query Match
Best Local S
Matches 4
                                                                                                                                                                                                                                                                                 polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II) The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The
                                                                                                                                                                            diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                            Sequence
                                                                                                                                                                                                                                                     amino acid sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drmanac
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23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAR-2001; 2001WO-US08631.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human diagnostic protein #30223
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 511 WVYWVP 516
                                                                      Local Similarity
nes 4; Conserv
                                  1 WLYWIP 6
                                                                                                                                                                                                                                                     to produce other types of data and products dependent on DNA and so acid sequences. ABG00010-ABG30377 represent novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention relates to isolated polynucleotide (I) and
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                                                                                                                                            534
                                                                      Conservative
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                                                                                     90.98;
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                                                                    Score 40; DB Pred. No. 84; 2; Mismatches
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                                                                                                                                                                                                                                                 represent novel human
                                                                                                      22;
                                                                    0;
                                                                                                      Length 534;
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                                                                    Gaps
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RESULT 8
ABB67564
ID ABB6
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AAU32016
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PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid in treatment of leukaemias. AAU29510-ABU33304 represent the amino acid
                                                                                                                                                                          Matches
                                                                                                                                                                                     Query Match
Best Local
                             ABB67564 standard; Protein;
                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU32016;
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АВВ67564;
                                                                                                                                                                                                                                                                   sequences of novel human secreted proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20; Page 541; 765pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-611725/70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             stem cell proliferation; haematopoiesis; nerve tissue regeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; vaccination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human secreted protein #2507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                           511 WVYWVP 516
                                                                                                                                          1 WLYWIP 6
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                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                     534 AA;
                                                                                                                                                                          Conservative
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2001US-0770160
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                                                                                                                                                                                       90.9%;
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                             142
                                                                                                                                                                      Score 40; DB Pred. No. 84; 2; Mismatches
                                                                                                                                                                                                                                                                     of the invention
                                                                                                                                                                                                      22;
                                                                                                                                                                      0;
                                                                                                                                                                                                    Length 534;
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XZ

26-MAR-2002

(first entry)

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RESULT 9
AAU00427
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Best Local S
Matches 5
                                                                                                      Omega-3 fatty acyl desaturase; fat-1; omega-6 fatty acid; lipid; omega-3 fatty acid; omega-3 desaturase activity; food; oil; nutritional supplement; chemical feedstock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
                                       Region
                                                                               Caenorhabditis
                                                                                                                                                          Caenorhabditis elegans omega-3 fatty acyl desaturase fat-1 polypeptide
                                                                                                                                                                                     11-MAY-2001
                                                                                                                                                                                                               AAU00427;
                                                                                                                                                                                                                                       AAU00427 standard; Protein; 402 AA
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence data for this patent did not form specification, but was obtained in electronic at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 29484; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid genes from Drosophila and interactions -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PEKE ) PE CORP NY
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                         53 WRYWIP
                                                                                                                                                                                                                                                                                                                                                          Local Similarity
les 5; Conserv
                                                                                                                                                                                                                                                                                                                                1 WLYWIP 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention relates to an isolated nucleic acid detection reagent
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DB; ABL11667.
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                                                                                                                                                                                    (first entry)
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2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                                                              AA;
                                                                            elegans
                                      Location/Qualifiers 80..124
                           /note-
                                                                                                                                                                                                                                                                                                                                                                     86.4%;
"Region containing stretches of hydrophobic residues similar to those found in other desaturases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , DWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   detection reagent for detecting 1000 for elucidating cell signalling and c
                                                                                                                                                                                                                                                                                                                                                     Score 38; DB Pred. No. 48; 0; Mismatches
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RESULT 10
AAE22532
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22- Carbon fatty acids. Recombinant expression of C. elegans fat-1 polynucleotide in a wide variety of host cells, including Arabidopsis thaliana and Saccharomyces cerevisiae, produces a polypeptide with omega-3 desaturase activity. A host cell transformed with C. elegans fat-1 polynucleotide is useful for desaturating an omega-6 fatty acid to an omega-3 fatty acid by growing the host cell under conditions under which the polypeptide is expressed. The fat-1 polypeptide is useful for producing lipids having a higher proportion of omega-3 fatty acid and the lipids are useful as food, oils, as nutritional supplements, and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acyl desaturase fat-1 polypeptide. The polypeptide desaturates omega-6 fatty acid to a corresponding omega-3 fatty acid by catalysing the introduction of an omega-3 double bond into 18-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel host cell transformed with recombinant fat-1 polynucleotide encoding polypeptide which desaturates omega-6 fatty acid to corresponding omega-3 fatty acid, useful for producing lipids -
Caenorhabditis elegans fat-1 (omega-3 fatty acyl desaturase) protein.
                                                    26-JUL-2002
                                                                                                        AAE22532;
                                                                                                                                                         AAE22532 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chemical teedstocks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 1; 17pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US6194167-B1
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                                                                                                                                                                                                                                                                                            261 WYYWVP 266
                                                                                                                                                                                                                                                                                                                                                1 WLYWIP 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001-217927/22
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                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       402
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                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97US-0038409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0025578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           324
/note=
327..32
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162..163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note=
159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123
/note= "Highly conserved in
127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       229..284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note=
                                                                                                                                                            Protein; 402
                                                                                                                                                                                                                                                                                                                                                                                                                          86.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      represents Caenorhabditis elegans omega-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Highly conserved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Highly conserved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        desaturases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Region containing residues similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Highly conserved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Highly conserved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Highly
                                                                                                                                                                                                                                                                                                                                                                                               Score 38; DB 22;
Pred. No. 1.3e+02;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     conserved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FOUND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         membrane desaturases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 membrane desaturases"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 402;
                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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Best Local
                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                               01575
                                                                                                                                fungal infection;
epithelial cell pi
                                                                                                                                          Human secreted protein; autoimmune disorder; hyperproliferative cardiovascular disorder; cerebrovascular disorder; angiogenesis; nervous system disorder; bacterial infection; viral infection; fungal infection; ocular disorder; wound healing; tissue regener
                                                                                                                                                                                                                                                                    AAU01575 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant expression of fat-1 gene of Caenorhabditis elegans in wide variety of cells, including cells of Arabidopsis thaliana and Saccharomyces cerevisiae, produces a polypeptide having omega-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Browse
(HUMA-) HUMAN GENOME SCI INC
                                                                                                           Homo sapiens.
                                                                                                                                                                                                  Human secreted
                                                                                                                                                                                                                        18-JUL-2001
                                                                                                                                                                                                                                             AAU01575
                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is Caenorhabditis elegans FAT-1, an omega-3 fatty acyl desaturase protein. FAT-1 polypeptide is useful for producing lipids having a higher proportion of omega-3 fatty acid. Such lipids are useful as food oils nutritional supplements and as chemical feedstocks.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Fig 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    desaturase activity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-FEB-1997;
18-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US2002042933-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FAT-1 protein; omega-3 fatty acyl
food oil; nutritional supplement;
                      27-SEP-1999;
                                           26-SEP-2000; 2000WO-US26337
                                                                                      WO200123547-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BROW/) BROWSE J A.
(SPYC/) SPYCHALLA J P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-DEC-2000;
                                                                                                                                                                                                                                                                                                                           261 WYYWVP 266
                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                1 WLYWIP 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2002-361389/39.
DB; AAD35559.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JA,
                                                                                                                                                                                                                                                                                                                                                                       4;
                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-038409P
98US-0025578
                     99US-0155806
                                                                                                                                                                                                  protein immunogenic
                                                                                                                                 proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20pp;
                                                                                                                                                                                                                                                                   Peptide;
                                                                                                                                                                                                                                                                                                                                                                                  86.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English.
                                                                                                                                                                                                                                                                    27
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                                                                                                                                                                                                                                                                                                                                                                                Score
Pred.
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       desaturase; chemical feedstock;
                                                                                                                                                                                                 epitope encoded by
                                                                                                                                                                                                                                                                                                                                                                                            38;
                                                                                                                                                                                                                                                                                                                                                                               DB 23;
1.3e+02;
                                                                                                                                 chemotaxis;
                                                                                                                                                                                                                                                                                                                                                                                            Length 402;
                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                  gene
                                                                                                                                           regeneration;
                                                                                                                                                                                                  #15
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                                                                                                                                                                           disorder;
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RESULT 12
ABP28377
ID ABP28
XX ABP28
XX ABP28
XX O2-JU
DE Strep
XX Strep
XX Strep
XX Grup
CW antii
OX Strep
XX W0200
XX W200
X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence represents a human secreted protein encoded by a nucleic CC acid of the invention. Secreted proteins and their related nucleic acids CC can be used in the diagnosis of or susceptibility to a pathological CC condition by determining the presence or absence of a mutation in a nucleic acid or the presence or amount of expression of a secreted CC protein. The sequences are used to prevent, treat or ameliorate a medical CC condition in e.g. humans, mice, rabbits, goats, horses, catts, dogs, CC chickens or sheep. The antibodies to the polypeptides can also be used in CC calleviating symptoms associated with disorders and in diagnostic communoassays e.g. radioimmunoassays or enzyme linkedCC immunoassays e.g. radioimmunoassays or enzyme linkedCC immunoassays e.g. radioimmunoassays or enzyme linkedCC immunoassays or creative disorders e.g. neophasms of the breast or CC arthitis, hyperproliferative disorders e.g. neophasms of the breast or CC iver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular CC disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and CC used to aid wound healing and epithelial cell proliferation, to help or transplantation to regenerate tiscuse in chemetaris and as a food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                       27-OCT-2000;
24-NOV-2000;
07-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding 26 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. Gaucher's disease, Alzheimer's disease, Scimitar syndrome, Creutzfeldt-Jacob disease, Alzheimer's disease, Scimitar syndrome, Creutzfeldt-Jacob disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 387;
                                                                                                                                                                                                            29-OCT-2001; 2001WO-GB04789
                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus agalactiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP28377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABP28377 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                additive or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diabetes mellitus and multiple sclerosis
                            (CHIR-) CHIRON SPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transplantation,
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(GENO-) INST GENOMIC RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 WLYWIP 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   preservative
                                                                                       2000GB-0026333.
2000GB-0028727.
2001GB-0005640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to regenerate tissues, in chemotaxis and as a food ervative to alter storage capabilities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
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13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
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Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds t (I). A composition comprising (I) or a nucleic acid encoding (I), may used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treatted may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromotography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                              Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment of the second of the manufacture of medicaments for
                N-PSDB;
                                                        Venter
                                                                                                               23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster polypeptide SEQ
                                                                                                                                                                                                                                                                                                                                                26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                            ABB60764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 3755; 4525pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
                                                                                                                                                         23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                       27-SEP-2001
                                                                                                                                                                                                                   WO200171042-A2
                                                                                                                                                                                                                                                                          pharmaceutical.
                                                                                                                                                                                                                                                                                          Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                     ABB60764 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus proteins.
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                                                                                   (PEKE )
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                ABL04867
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                                                       Adams M,
                                                                                                                                                                                                                                                                                      developmental biology;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
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100.0%;
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Pred. No.
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                                                                                                                                                                                                                                                                                      cell signalling; insecticide;
                                                        EW;
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1.9e+02;
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Best Local :
        AAU03601-AAU03722 represent Group B Streptococcus (Streptococcus agalactiae) amino acid sequences of the invention. S. agalactiae is an encapsulated bacterium which is a major pathogen of humans causing sepsis and meningitis in neonates as well as adults. The S. agalactiae antigenic polypeptides are used to vaccinate against Group B Streptococcus infections, particularly to prevent infection in new born children
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB577737-ABB72072).
                                                                                                                                               New polypeptides derived from Streptococcus agalactiae are useful to provide detection of, and vaccination against, Group B Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                            Group B Streptococcus; encapsulated bacterium; therapeutic; sepsis
meningitis; neonate; antigenic; vaccine; infection; genital tract;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cel
                                                                                                           Claim
                                                                                                                                                                                                                                      ē
                                                                                                                                                                                                                                                                                                                     07-SEP-2000; 2000WO-GB03437
                                                                                                                                                                                                                                                                                                                                                                           WO200132882-A2
                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus agalactiae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              specification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       capable of detecting 1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 9084; 21pp + Sequence Listing;
                                                                                                                                                                                                                                                              (MICR-) MICROBIAL TECHNICS LTD
                                                                                                                                                                                                                                                                                                                                                10-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence data
                                                                                                                                  infections, particularly to prevent infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          360 WLYWKP 365
                                                                                                                                                                                                                                   Page
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention relates
                                                                                                                                                                                                          2001-316444/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ħ
                                                                                                        1; Fig 1; 178pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                               polysaccharide vaccination.
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5; Conserv
                                                                                                                                                                                                                                    RWF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus antigenic protein,
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                                                                                                                                                                                                                                    Wells
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                                                                                                                                                                                                                                    Hanniffy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     an isolated nucleic acid detection ror more genes from Drosophila. The
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RESULT 15
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                                                          Query Match
                                                                                                    The sequence was deduced from a cloe isolated from a cDNA library prepd. from peripheral T cell poly(A)+ mRNA. The gene can be used to express recombinant PTPase or derivs. useful in cancer therapy where a protein kinase is involved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
Region
                                                                                 Sequence
                                                                                                                                                              Disclosure; Fig 1; 38pp; English.
                                                                                                                                                                                     tyrosine phosphatase.
                                                                                                                                                                                               New DNA encoding non-receptor-linked protein tyrosine ohosphatase used in treating malignancies associated with protein-linked
                                                                                                                                                                                                                                  WPI; 1991-295643/40.
N-PSDB; AAQ13802.
                                                                                                                                                                                                                                                                     Fischer EH,
                                                                                                                                                                                                                                                                                            (WASH-) WASHINGTON RES FOUN.
                                                                                                                                                                                                                                                                                                                   14-MAR-1990;
                                                                                                                                                                                                                                                                                                                                         14-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                       WO9113989-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Non-receptor linked protein tyrosine phosphatase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful in the preparation of a medicament for the treatment or prophylaxis of Group B Streptococcus infection. The invention does not have the disadvantages of varied response rate associated with prior art capsid polysaccharide vaccination against Group B Streptococcus.
                                                                                                                                                                                                                                                                                                                                                                19-SEP-1991.
1 WLYWIP 6
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nes 5; Conserv
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ilarity 100.0%; Pred. No. 1.9e+02;
Conservative 0; Mismatches 0;
                                    Conservative
                                                                                                                                                                                                                                                                     Krebs EG,
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                                                                                                                                                                                                                                                                                                                                         91WO-US01748
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= core region 377..381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers 42..274
                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= nuclear recognition signal
396..415
                                                                                                                                                                                                                                                                                                                                                                                                                        /label=
                                                                                                                                                                                                                                                                                                                                                                                                              /note= "hydrophobic"
                                            84.1%;
                                                                                                                                                                                                                                                                     Tonks NK,
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                                 Score 37; DB 12
Pred. No. 2e+02;
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                 hypothetical prote ubiquitin-binding arachidonate 12-li arachidonate 12-li arachidonate 12-li hypothetical prote hypothetical prote hypothetical prote hypothetical prote protein-tyrosine-pamino acid transpor membrane transport bicaudal-C- fruit
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MGA1 protein - yea
2-oxyglutarate/mal
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Query Match 90.9%; Score 40; DB 2; Length 533; Best Local Similarity 66.7%; Pred. No. 39;	RESULT 2 T00742 ubiquitin-binding protein homolog A-735G6.2 - human C;Species: Homo sapiens (man) C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 23-Mar-20 C;Accession: T00742 R;Adams, M.D.; Loftus, B.J.; Zhou, L.; Crosby, M.; Fuhrmann, J.; Brandon, submitted to the EMBL Data Library, March 1998 A;Description: Human Chromosome 16 BAC clone CIT987SK-A-735G6. A;Reference number: Z14181 A;Accession: T00742 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-533 <ada> A;Residues: 1-533 <ada> A;Cross-references: EMBD:AC002400; NID:g2576344; PIDN:AAC05812.1; PID:g25 C;Genetics: A;Gene: A-735G6.2 A;Note: A-735G6.2</ada></ada>	1 MIXMIP 6 1 HIH:  3257	95.5%; Score 42; DB 2; Length 3944; milarity 83.3%; Pred. No. 1.2e+02; Conservative 1. Mismatches 0. Indels 0. Car	2 35 79.5 47.3 2 LD44/51 2 35 79.5 528 2 S26948 3 579.5 538 2 S36424 4 35 79.5 541 1 ODZJ1 5 35 79.5 541 2 A48327  ALIGNMENTS  T 1 7 1 7 1 7 1 7 1 7 1 8 1	lla het het ho- ho- het
	8-Mar-2001 Brandon, R.; Kim, U.	  	Gaps	come-c oxida	syntein ein protein protein protein protein protein protein protein cane

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A;Cross-references: EMBL:L06040; NID:g205212; PIDN:AAA41532.1; PID:g205213 C;Superfamily: arachidonate 5-lipoxygenase C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                   C;Accession: $30051
R;Watanabe, T.; Wedina, J.F.; Haeggstroem, J.Z.; Radmark, Eur. J. Biochem. 212, 605-612, 1993
A;Title: Molecular cloning of a 12-lipoxygenase cDNA from A;Reference number: $30051; MUID:93185682; PMID:8444196
A;Accession: $30051
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A:Residues: 1-36,'N',38-118,'Q',120-396,'N',398-663 <RES>
A:Cross-references: GB:L34570; NID:g509607; PIDN:AAA64930.1; PID:g763530
C:Comment: A second arachidonate 12-11poxygenase from mouse platelets is
C:Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ross-references: GB:U04331; NID:g467216; PIDN:AAA20658.1; PID:g467217
"Experimental source: strains C57BL/6 and ICR, spleen leukocytes
A:Note: removal or substitution of I1e-663 abolished enzyme activity
R;Freire-Moar, J; Alavi-Nassab, A.; Ng, M.; Mulkins, M.; Sigal, E.
Biochim. Biophys. Acta 1254, 112-116, 1995
A;Title: Cloning and characterization of a murine macrophage lipoxygenase.
A;Reference number: 149439; MUID:95110857; PMID:7811740
A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 arachidonate 12-lipoxygenase (EC 1.13.11.31), leukocyte [validated] - mouse C:Species: Mus musculus (house mouse) C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000 C:Accession: B54075; 149439
R:Chen, X.S.; Kurre, U.; Jenkins, N.A.; Copeland, N.G.; Funk, C.D.
J. Biol. Chem. 269, 13979-13987, 1994
A:Reference number: A54075; MUID:94245713; PMID:8188678
A:Accession: B54075
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A; Residues: 1-663 <WAT>
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C; Superfamily: arachidonate 5-lipoxygenase
C; Keywords: oxidoreductase
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C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S30051
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Residues: 1-663 <CHE>
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hypothetical protein Y53C10A.9 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000 C;Accession: T27121 R;White, S
                                                                                                                                     R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, Lory, S.; Olson, M.V.; Lory, S.; Olson, M.V.; Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1564 <WIL>
A;Cross-references: EMBL:ALO33536; PIDN:CAA22142.1; CESP:Y53C10A.
A;Experimental source: clone Y53C10A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:S69383; NID:g545793; C;Superfamily: arachidonate 5-lipoxygenase C;Keywords: oxidoreductase
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A;Title: Arachidonate 12-lipoxygenase of rat pineal glands: catalytic properties A;Reference number: I52462; MUID:94162305; PMID:8117750
A;Accession: I52462
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C;Species: Rattus sp. (rat)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 11-Jun-1999
                                                                A; Reference number: A; Accession: C83360
                                                                                                                                                                                                                                                     C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision
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C;Superfamily: unassigned
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A; Molecule type: DNA
A; Residues: 1-211 <STO>
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A; Residues: 1-663 < RES>
                                             A;Status: preliminary
                                                                                                           A; Title: Complete genome
                                                                                                                                                                                                                                                                                                hypothetical protęin PA2287 [imported] - Pseudomonas aeruginosa (strain PAO1)
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                                                                                          sequence of Pseudomonas aeruginosa PAO1, 50; MUID:20437337; PMID:10984043
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A.; Larbig,
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K.; L
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GB:AE004654; GB:AE004091; NID:g9948311; PIDN:AAG05675.1; GSPDB:GN

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A;Status: pace...
A;Molecule type: DNA
A;Residues: 1-739 <WIL>
A;Cross-references: EMBL:Z68220; P!
A;Cross-references: Clone T20D3
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                                                                                                                                                                     A; Map position: 4
A; Introns: 205/1; 246/3; 437/2; 472/1; 643/3; 721/2
C; Superfamily: Caenorhabditis elegans hypothetical |
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A;Molecule type: DNA
A;Residues: 1-407 <SCH>
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C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change
C;Accession: T48817
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A;Reference number: Z19971
A;Accession: T25030
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A; Introns: 56/2; 68/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: C; Genetics:
                                                                                                                                                                                                                 A; Gene: CESP:T20D3.11
                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein T20D3.11 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: NCSP: 68B2.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:AL353821; GSPDB:GN00112; NCSP:68B2.10
A;Experimental source: cosmid contig 68B2; strain 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, mitted to the Protein Sequence Database, April 2000 Reference number: 24541
A;Accession: T48817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein 68B2.10 [imported] - Neurospora crassa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T48817
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                                                                                                                                                                   Superfamily:
                                                                                                                                                                                                                                                                                                               Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                               Species: Caenorhabditis elegans
Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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loyd, C.
                                     475 WSYWIP 480
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hes 4; Conserv
                                                                                                                    Local
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5; Conser
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66.7%;
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66.7%;
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                                                                                                                                 Score 38;
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Pred. No.
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Pred. No.
                                                                                                                  Pred. No.
                                                                                                    Mismatches
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                                                                                                                                                                  hypothetical protein T20D3
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62;
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33;
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                                                                                                                                 DB 2; Length 739;
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AF1079
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A;Cross-references: GB:NC_003210; PIDN:CAC98252.1; PID:g16409396; GSPDB:GN00177
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D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AF1079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GDB:128098; OMIM:176887
A;Map position: 18p11.22-18p11.21
A;Introns: 120/3; 165/3; 235/3; 347/2
A;Note: list of introns may be incomplete
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 1; protein-tyrosine-C;Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase;
C;Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase;
F;42-264/Domain: protein-tyrosine-phosphatase homology cPTP>
F;216/Active site: Cys (phosphocystaine intermediate) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 348-415 <CHA>
A;Residues: G148-415 <CHA>
R;Johnson, C.V.; Cool, D.E.; Glaccum, M.B.; Green, N.; Fischer, E.H.; Bruskin, A.;
Genomics 16, 619-629, 1993
A;Title: Isolation and mapping of human T-cell protein tyrosine phosphatase sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C:Species: Homo sapiens (man)
C;Date: 31-War-1990 #sequence_revision 02-May-1994 #text_change 07-May-1999
C;Accession: A3399; C60345; A45742
R:Cool, D.E.; Tonks, N.K.; Charbonneau, H.; Walsh, K.A.; Fischer, E.H.; Krebs, E.G.
Proc. Natl. Acad. Sci. U.S.A. 86, 5257-5261, 1989
A:Title: CDNA isolated from a human T-cell library encodes a member of the protein-ty A;Reference number: A33899; MUID:89315776; PMID:2546150
A;Accession: A33899;
A; Molecule type: DNA
A; Residues: 1-461 <GLA>
                                                                                                                                                                                                                                                                                                                R;Glaser, P.; Frangeul, L.; .; Dominguez-Bernal, G.; Du
                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 115-125; 160-170; 230-241; 413-415 < JOH>
C; Comment: This protein and protein-tyrosine-phos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Reference number: A45742; MUID:93315152; PMID:8325634
A;Accession: A45742
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
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R;Champion-Arnaud, P.; Gesnel, M.C.; Foulkes, N.; Ronsin, C.; Sassone-C Oncogene 6, 1203-1209, 1931
A;Title: Activation of transcription via AP-1 or CREB regulatory sites A;Reference number: A60345; MUID:91319401; PMID:1650442
A;Accession: C60345
                                                              A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                               C; Accession: AF1079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid transporter homolog lmo0037 [imported] - Listeria monocytogenes (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: GDB: PTPN2; PTPT
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A; Residues: 1-415 <COO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
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les 5; Conserv
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                                                                                                                                                                                                                                                                                                                   Duchaud,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84.1%;
83.3%;
                                                                                                                                                                                                                                                                                                                   Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; chaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein-tyrosine-phosphatase 11A
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Pred. No.
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(Arg) #status predicted
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pester hydrolase; tyr
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C;Species: Drosophila melanogaster
C:Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 29-May-1998
Accession: S55051
A;Title: Localized Bicaudal-C RNA encodes a protein containing a KH domain, A;Reference number: S55051; MUID:95262644; PMID:7538070
A;Accession: S55051
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A;Introns: 19/3
C;Superfamily: amiloride resistance protein carl
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C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
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                                                                                                                                     A;Cross-references: FlyBase:FBgn0000182
A;Introns: 118/3; 142/1; 168/3; 277/3;
C;Superfamily: SAM homology
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A; Experimental source:
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A; Residues: 1-525 <WOO>
                                                                                                                          F;800-865/Domain:
                                                                                                                                                                                    A;Gene: FlyBase:BicC
                                                                                                                                                                                                    C; Genetics
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A; Residues: 1-938 <MAH>
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                                                                                                                                                                                                                                                              A; Status: preliminary
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Dood, V.; Rajandream, M.A.; Barrell, B.G.; Murphy, litted to the EMBL Data Library, September 1998
Reference number: Z21954
;Accession: T41427
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Best Local
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nes 5; Conserv
30 WIHWIP 35
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5; Conserv
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100.0%; Pr
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Pred. No.
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                                                                                                                                                       319/3; 447/1;
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2e+02;
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1e+02;
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A; DELOWN, S.D.; Twells, R.C.J.; Hey, P.J.; Cox, R.D.; Levy Biochem. Biophys. Res. Commun. 248, 879-888, 1998
A;Title: Isolation and characterization of IRP6, a novel A;Reference number: JE0272; MUID:98369644; PMID:9704021
A;Accession: JE0273
A;Moleculo turn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Map position: 12p11-12p13
C; Superfamily: low density lipoprotein receptor-related
F; 286-323, Domain: EGF homology <EGF1>
F; 592-627, Domain: EGF homology <EGF2>
F; 1207-1243/Domain: LDL receptor ligand-binding repeat F; 1249-1285/Domain: LDL receptor ligand-binding repeat F; 1288-1322/Domain: LDL receptor ligand-binding repeat F; 1286-1360/Domain: LDL receptor ligand-binding repeat F; 1326-1360/Domain: LDL receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position: 6
C; Superfamily: low density lipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          low density lipoprotein receptor-related protein 6 - mouse C;Species: Mus musculus (house mouse) C;Decies: Mus musculus (house mouse) C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 02-Aug-2002 C;Accession: JE0273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δõ
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A;Title: Isolation and characterization of LRP6, a novel A;Reference number: JE0272; MUID:98389644; PMID:9704021
밁
                                                                                                Query Match
Best Local Similarity
Thehes 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                              F;286-323/Domain: EGF homology <EGF1>
F;592-627/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: Lrp6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Genetics:
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A; Residues: 1-1613 <B
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A; Residues: 1-1613 <BRO>
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C; Species: Homo sapiens (man)
C; Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 02-Aug-2002
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1156 WLYWI 1160
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3.3e+02;
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3.3e+02
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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      SwissProt_40:*
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AQP4_MOUSE
AQP4_BOVIN
                                                                                                                                                                                                                                                                                                                         AQY1_YEAST
MRAY_HAEIN
CSG2_YEAST
MMUP_ECOLI
ROCE_BACSU
COX1_TRIRU
COX1_RHILE
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LOXL_MOUSE
CATS_MOUSE
PTN2_HUMAN
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AQP4_RAT
YBL4_YEAST
VAL1_YEAST
TESK_MOUSE
HAK1_DEBOC
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Best Local :
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                                                                                                                                                                                                                                                                                                      MEDLINE=94245713; PubMed=8188678; Chen X.-S., Kurre U., Jenkins N.A., Copeland N.G., Funk C.D.; "CDNA cloning, expression, mutagenesis of C-terminal isoleucine, genomic structure, and chromosomal localizations of murine 12-lipoxygenases.";
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15-JUN-2002 (Rel. 41, Last annotation update)
Arachidonate 12-lipoxygenase, leukocyte-type
ALOX12L OR ALOX15.
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                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
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MEDLINE-95110857;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                          PATHWAY: Leukotrienes biosynthesis.
SUBCELLULAR LOCATION: Cytoplasmic.
TISSUE SPECIFICITY: FOUND IN PITUITARY AND PINEAL
                                                                                       SIMILARITY: BELONGS TO THE LIPOXYGENASE FAMILY
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an email to license@isb-sib.ch).
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EMBL; L34570;
HSSP; P12530;
    Dandoy-Dron F., Guillo F., Benboudjema L., Deslys J.-P., Lasmesas Dormont D., Tovey M.G., Dron M.;
"Gene expression in scrapie. Cloning of a new scrapie-responsive and the identification of increased levels of seven other mRNA transcripts.";
Transcripts.";
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                                                           STRAIN=C57BL/6; TISSUE=Brain; MEDLINE=98184882; PubMed=9516475;
                                                                                 SEQUENCE OF 296-340 FROM N.A.
                                                                                                      Biochim.
                                                                                                                                   Soederstroem M., Salminen H., Glumoff V.,
                                                                                                                                                       SEQUENCE OF 144-306 FROM N.A.,
STRAIN-C57BL/6; TISSUE-Cartilac
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InterPro; IPR000907; Lipoxygenase.
InterPro; IPR001024; Lipoxygenase_LH2.
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InterPro; IPR000169; SHprot_acsite.
Pfam; PF00112; Peptidase_C1; 1.
PRINTS; PR00705; PAPAIN.
PRODOM; PD000158; Peptidase_C1; 1.
PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
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BL; AF051731; AAC05781.1; JOINED.
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SUBCELLULAR LOCATION: Lysosomal.
TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST EXPRESSION FOUND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATHEPSIN N.
CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: THIOL PROTEASE. THE BOND-SPECIFICITY OF THIS PROTEINASE IS IN PART SIMILAR TO THE SPECIFICITIES OF CATHEPSIN L AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IN NON-SKELETAL TISSUES. RELATIVELY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through
een the Swiss Institute of Bioinformatics and the EN
                  WLYWIP 6
                                                                                                                                                                                                                                                                                                                                                                       MGI:107341; Ctss.
WLFWMP
                                                                                                                                                                                                                                                                                                                                                                                           P25774;
                                                                                                                                                                                                                                                                                                                                                                                                              AF038546; AAB94925.1;
AJ002386; CAA05360.1;
Y18466; CAA77184.1;
                                                                                                                                                                                                                                                                                                                                                                                                     AJ223208;
                                                 Similarity
                                                                            34
97
106
146
340
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113
113
147
287
307
307
134
178
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120
218
                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                            1BXF.
                                                                                                                                                                                                                                                                            protease;
                                                                                                                                                                                                                                                                                      THIOL_PROTEASE_ASN;
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340
147
287
307
233
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97
106
                                                                              38438 MW;
                                                84.1%;
66.7%;
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                                      2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is not removed.
                                               Score
Pred.
                                                                                    MRAPGHAAIRWLFWMPLVCSVAMEQLQRD -> MAVLDAPG VLCGNGATAER (IN REF. 2).
Y -> H (IN REF. 2).
S -> L (IN REF. 2).
S -> P (IN REF. 2).
A -> S (IN REF. 3).
                                                                                                                                                    N-LINKED (GLCNAC. . T -> M.
                                                                                                                                                                                                                                   CATHEPSIN S.
BY SIMILARITY.
                                                                                                                                                                                                                                                        ACTIVATION PEPTIDE (POTENTIAL).
                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                     Y SIMILARITY.
Y SIMILARITY.
Y SIMILARITY.
                                                                             068E61126E2E0C0E CRC64;
                                                                                                                                                                                 SIMILARITY
SIMILARITY
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                                      Mismatches
                                                                                                                                                                         SIMILARITY
                                                37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cathepsin
                                                                                                                                                                                                                                                                            Zymogen; Signal.
                                             DB
23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         more
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Usage
                                     0;
                                                       Length 340;
                                                                                                                                                             .) (FOTENTIAL).
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the Z-Val-Val-
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RESULT

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ALD PACES OF THE PROPERTY OF T
                                          DOMAIN
ACT_SITE
VARSPLIC
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SMART; S
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EMBL; M81478; -; NOT_ANNOTATED_CDS.
EMBL; BC008244; AAA08244.1; -.
PIR; A33899; A33899.
HSSP; P18031; 1PTY.
Genew; HGNC:9650; PTPN2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed: entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-89315776; PubMed-2546150;
Cool D., Tonks N., Charbonneau H., Walsh K., Fische
"CDNA isolated from a human T-cell library encodes
protein-tyrosine-phosphatase family.";
Proc. Natl. Acad. Sci. U.S.A. 86:5257-5261(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTN2_HUMAN STANDARD; PRT; 415 AA. P17706; Q96HR2; 01-AUG-1990 (Rel. 15, Created) 01-AUG-1990 (Rel. 15, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Protein-tyrosine phosphatase, non-receptor type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HUMAN
                                                                                                                                                                                                                                     InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000242; TYI_P.
Pfam; PF00102; Y_phosphatase; 1.
PRINTS; PR00700; PRTYPHPHTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein-tyrosine-phosphatase.";
Proc. Natl. Acad. Sci. U.S.A. 89:499-503(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cell protein-tyrosine PTPN2 OR PTPT.
  SEQUENCE
                                                                                                                                     SMART: SMO0194: PTPC; 1.

PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.

PROSITE: PS50056; TYR_PHOSPHATASE_PTP; 1.

PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAY-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mosinger B. Jr., Tillmann U., "Cloning and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                      Hydrolase;
                                                                                                                                                                                                                                                                                                                                             MIM; 176887;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Eye;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=92115688; PubMed=1731319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Cytoplasmic.
SUBCELLULAR LOCATION: Cytoplasmic.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; PTPA
PRODUCED BY ALTERNATIVE SPLICING.
PISSUE SPECIFICITY: PTPA ISOFORM IS PROFESSED IN HUMAN TISSUES. PTPB ISOFOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "...ced (MAY-2001) to the EMBL/GenBank/DDBJ databases.
CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = tyrosine + phosphate.
Graper running.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS TYROSINE PHOSPHATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IN PLACENTA.
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216
382
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  AA;
                    Alternative splicing.
286 PROTEIN-TYGOSINE PHOSPHATASE.
216 BY SIMILARITY.
415 WLYMOPILTENMGFMSVILVGAFVGWRLFFQQNAL ->
TDT (IN ISOFORM PTPA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ISOFORM PTPB).
48528
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  MW;
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Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Westphal H., Tre of a mouse cDNA
  0599694A4F058E68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IS PROBABLY
ISOFORM WAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fischer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAJOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N
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DEPTOAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 5; Conserv
                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (LONG ISOFORM).
MEDLINE-94363219; PubMed-8081734;
Yamamoto-Hino M., Sugiyama T., Hikiti K.,
Hasegawa K., Sekine S., Sakurada K., Miyaw
Hasegawa M., Mikoshiba K.;
"Cloning and characterization of human typ.
1,4,5-trisphosphate receptors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IP3S_HUMAN STANDARD; PRT; 2701 AA. Q14571; O94773; O1-NOV-1997 (Rel. 35, Created) O1-NOV-1997 (Rel. 35, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Inositol 1,4,5-trisphosphate receptor type 2 (Type 2 inositol trisphosphate receptor) (Type. 2 Insp3 receptor) (IP3 receptor) (Insp3R2).
              Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Futateugi A., Kuwajima G., Mikoshiba K.;
"Muscle-specific mRNA isoform encodes a protein composed m
N-terminal 175 residues of type 2 Ins(1,4,5)P3 receptor.";
Biochem. J. 334:559-563(1998).
                               EMBL; AB012610;
                                            EMBL; D26350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98399819; PubMed=9729462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (SHORT ISOFORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   382 WLYWOP 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 WLYWIP 6
                                                                                                                                                                                                    DOMAIN: THE RECEPTOR CONTAINS A CALCIUM CHANNEL IN ITS C-EXTREMITY. ITS LARGE N-TERMINAL CYTOPLASMIC REGION HAS TH BINDING SITE IN THE N-TERMINUS AND MODULATORY SITES IN THE PORTION IMMEDIATELY UPSTREAM OF THE CHANNEL REGION. PTM: PHOSPHORYLATED ON TYROSINE RESIDUES (BY SIMILARITY). MISCELLANBOUS: CALCIUM APPEARS TO INHHIT LIGAND BINDING RECEPTOR, MOST PROBABLY BY INTERACTING WITH A DISTINCT CALCIUM-BINDING PROTEIN WHICH THEN INHIBITS THE RECEPTOR. SIMILARITY: BELONGS TO THE INSP3 RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                  ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN I SHORT FORM/TIPR; ARE PRODUCED BY ALTERNATIVE SPLICING TISSUE SPECIFICITY: THE SHORT ISOFORM IS FOUND IN SKE
                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: RECEPTOR FOR INOSITOL 1,4,5-TRISPHOSPHATE, MESSENGER THAT MEDIATES THE RELEASE OF INTRACELLULAR SUBUNIT: HONOTETRAMER (BY SINILARITY).
SUBCELLULAR LOCATION: Integral membrane protein. Endc
                                                                                                                                                                                                                                                                                                                                                        AND HEART
 600144;
              HGNC:6181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                            BAA05384.1;
                               BAA33961.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2:9-22(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.1%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Eutelo
Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human type 2 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Miyawaki A.,
                                                                                           (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mattei M.-G
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                                                                                                                                                                                                                                                                                                                                                                                                    (SHOWN HERE) AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Furuichi T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Endoplasmic
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                                                                                                                                          restrictions
                                                                                                            and
                                                                                                                                                          EMBL
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S THE LIGAND-
N THE MIDDLE
                                                                                                                                                              a collaboration

MBL outstation -
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isoform
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RESULT 6
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Best Local S
Matches 5
                STRAIN-Sprague-Dawley;
Magnino F., Dufour J.-F.;
"New rat IP3R isoform 2 sequence.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: RECEPTOR FOR INOSITOL 1,4,5-TRISPHOSPHATE,
MESSENGER THAT MEDIATES THE RELEASE OF INTRACELLULAR
                                                                                                                                                                                                                                                 TP3S_RAT STANDARD; PRT; 2701 AA.
P29995; Q99956;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Inositol 1,4,5-trisphosphate receptor type 2 (Type 2 inositol 1,4,5-trisphosphate receptor type 2 (Type 2 inositol 1,4,5-trisphosphate receptor) (Type 2 InsP3 receptor) (IP3 receptor isoforn 2) (InsP3R2).
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VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00520; ion_trans; 1. Pfam; PF01365; RYDR_ITPR; 2. Pfam; PF02815; MIR; 4.
                                                                                                           "Structure of a novel InsP3 receptor."; EMBO J. 10:3199-3206(1991).
                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001682; Ca/Na_pore.
InterPro; IPR000493; Insp3_receptor
InterPro; IPR000365; M-channel_nlg.
InterPro; IPR003608; MIR.
                                                                                     SEQUENCE FROM N.A
                                                                                                                                Mignery G.A.;
                                                                                                                                        Suedhof T.C.,
                                                                                                                                                      MEDLINE=92007769;
                                                                                                                                                                TISSUE=Brain;
                                                                                                                                                                                                                               Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Receptor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00779;
                                                                                                                                                                         SEQUENCE FROM N.A.,
                                                                                                                                                                                              NCBI_TaxID=10116
                                                                                                                                                                                                                                           ITPR2
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                                                                                                                                         Newton C.A.,
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                                                                                                                                                      PubMed=1655411;
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2701
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Rodentia;
                                                                                                                                                                           AND VARIANTS
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100.0%;
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Integral membrane
                                                                                                                                         Archer B.T.
                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MW.
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Pred. No.
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IVVGDK -> DASFWI (IN SHORT
MISSING (IN SHORT ISOFORM).
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Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                         III,
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1.6e+02;
                    OF INTRACELLULAR CALCIUM
                                                                                                                                                                                                          Vertebrata;
thi; Muridae;
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protein. Endoplasmic
                                                                                                                                         Ushkaryov Y.A.
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; Murinae; Rat
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RESULT 7
MGA1_YEAST
ID MGA1_YEAST STANDARD;
AC P53050;
DT 01-OCT-1996 (Rel. 34, Created)
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Pfam; PF01365; RYDR_ITPR; 2.
Pfam; PF02815; MIR; 4.
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InterPro; IPR000493; InsP3_receptor.
InterPro; IPR000636; M+channel_nlg.
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DOMAIN: THE RECEPTOR CONTAINS A CALCIUM CHANNEL IN ITS C-TERMINAL DOMAIN: THE RECEPTOR CONTAINS A CALCIUM CHANNEL IN ITS C-TERMINAL CYTOPLASMIC REGION HAS THE LIGAND-EXTREMITY. ITS LARGE N-TERMINUS AND MODULATORY SITES IN THE MIDDLE PORTION IMMEDIATELY UPSTREAM OF THE CHANNEL REGION.

PTM: PHOSPHORYLATED ON TYROSINE RESIDUES (BY SIMILARITY).

SIMILARITY: BELONGS TO THE INSP3 RECEPTOR FAMILY.
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                                                                                                                                                                                                                                   . Similarity 5; Conserv
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                                                                                                                                                                                                                                                      Score 37;
Pred. No.
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CYTOPLASMIC (POTENTIAL)
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-> R (IN REF. 2).
-> V (IN REF. 2).
-> G (IN REF. 2).
-> E (IN REF. 2).
42BF7F1024335984 CRC64;
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                                                                                                                                                                                                                                 Gaps
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      AC DT DT DT DT OS
                                                                                                                                                                    RESULT 8
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YQ21_CAEEL
Q09231;
Q1-NOV-1997
Q1-NOV-1997
Q1-NOV-1997
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-!- SUBCELLULAR LOCATION: Nuclear (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGD; S0003481; MGA1.
InterPro; IPR000232; HSF_DNA_bind
InterPro; IPR002341; HSF_ETS.
Pfam; PF00447; HSF_DNA-bind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi; //
Saccharomycetales;
NCBI_TaxID=4932;
                   Hypothetical C09F5.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00434; HSF_DOMAIN; 1. Nuclear protein; DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D29626; BAA06105.1; -.
EMBL; Y07703; CAA68970.1; -.
EMBL; Z73034; CAA97278.1; -.
HSSP; P2212; ZHTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=D416-1-4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast)
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MGA1 OR YGR249W.
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Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00415; HSF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00056; HSFDOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSFAC; T03496;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Feroli F., Carignani G., Pavanello A., Rodrigues-Pousada C., Melchioretto P.,
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22 WIYWSP 27
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456 AA;
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                                                                                                                                                                                                                                                                                                                                                                         50735 MW;
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                                    protein C09F5.1 in chromosome III
                                                                                          Created)
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Last annotation updat
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Last annotation update)
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Pred. No. 44;
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Panzeri L.,
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97464436; PubMed=9324257;
Ohnishi K., Fan F., Schoenhals G.J., Kihara M., Macnab
"The Flio, Flip, Filo, and Filis proteins of Salmonella
putative components for flagellar assembly.";
J. Bacteriol. 179:6092-6099(1997).
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P54702;
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                           the
                                                 between
                                                                                                                                                                                                Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-LT2 / SGSC1412 / ATCC 700720;
MEDLINE-21534948; PubMed-11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
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Bacteria; Proteobacteria;
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15-JUN-2002 (Rel. 41,
15-JUN-2002 (Rel. 41,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                          "Complete genome sequence of Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=602;
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                                                                                                                     SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO THE FLIR/MOPE/SPAR FAMILY.
                                                                                                                                                                    FUNCTION: ROLE IN FLAGELLAR BIOSYNTHESIS
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                           European
                   SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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Pred. No.
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RESULT 11
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RESULT 10
VG41_HSVI1
ID VG41_HSVI1
AC Q00117;
DT 01-DEC-1992 (Rel. 2
DT 01-DEC-1992 (Rel. 2
DT 01-DEC-1992 (Rel. 2
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TRANSMEM
TRANSMEM
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TRANSMEM
                                                                                                                                PIR;
                                                                                                                                                                             modified and this statement entities requires a license
                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                     "Channel catfish virus: a new type of herpesvirus."; Virology 186:9-14(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                          EMBL; M75136; AAA88144.1;
                                                                                                                                                                   entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                Davison A.J.;
                                                                                                                                                                                                                                                                                                                                                              Ictalurid Herpes-like viruses.
NCBI_TaxID=10401;
                                                                                                                                                                                                                                                                                                                                                                             Viruses; dsDNA viruses, Ictalurid Herpes-like v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                               Hypothetical
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MMYWDP
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41 protein.
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                                                 Score 35; DB Pred. No. 43; 1; Mismatches
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7AFF46906147A63F CRC64;
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43;
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Hall J., Hebling U., Heumann K., Hilbert H., Hillier L.,
Hunicke-Smith S., Hyman R., Johnston M., Kalman S., Kleine K.,
Komp C., Kurdi O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J.,
Marathe R., Messenguy F., Mewes H.-W., Mirtipati S., Moesti D.,
Marathe R., Messenguy F., Mewes H.-W., Mirtipati S., Moesti D.,
Mueller-Auer S., Namath A., Nentwich U., Oefner P., Pearson D.,
Petel F.X., Pohl T.M., Purnelle D., Schafer M., Scharfe M.,
Scherens B., Schramm S., Schroeder M., Sdicu A.M., Tettelin H.,
Urrestarazu L.A., Ushinsky S., Vierendeels F., Vissers S., Voss H.,
Walsh S.V., Wambutt R., Wang Y., Wedler E., Wedler H., Winnett E.,
The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";
Nature 387:103-105(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature
[2]
                                                                                                                                                                                                                                                Pfam; PF00230; MIP;
                                                                                                                                                                                                                                                                                           EMBL; U25841; AAB64
HSSP; P29972; 1FQY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between laboratory and wild-type strains.";
J. Biol. Chem. 273:27565-27572(1998).
-i- FUNCTION: WATER-SPECIFIC CHANNEL. SEEMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHARACTERIZATION.
MEDLINE=98438534; PubMed=9765289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansorge Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V., Botstein D., Bowman S., Bruckner M., Carpenter J., Cherry J.M., Chung E., Churcher C.M., Coster F., Davis K., Davis R.W., Churcher C.M., Coster F., Davis E., Duesterhoeft A., Dietrich F.S., Delius H., DiPaolo T., Dubois E., Duesterhoeft A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bussey H., Storms R.K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P53386;
01-OCT-1996
                                                               VARIANT
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                                                                                                                                                                                                                                                                  InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                    European Bioinformatics Institute.
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rPro; IPR000425; MIP_family.
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305
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PROSITE; P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MRAY_HAEIN STANDARD; PRT; 360 AA. P45062; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last seguence update) 15-JUN-2002 (Rel. 41, Last annotation update)
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TIGR; HI1135;
                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                           -i- FUNCTION: FIRST STEP OF THE LIPID CYCLE REACTIONS IN THE BIOSYNTHESIS OF THE CELL WALL PEPTIDOGLYCAN (BY SIMILARITY).
-i- CATALYTIC ACTIVITY: UDP-N-acetylmuramoyl-L-alanyl-D-glutamyl-L-lysyl-D-alanyl-D-alanine + undecaprenyl phosphate = UMP + N-acetylmuramoyl-L-alanyl-D-glutamyl-L-lysyl-D-alanyl-D-alanine-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
                                                                                                          PROSITE; PS01:
Peptidoglycan
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                                                                                                                                                    TIGR00445; mray;
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Dougherty B.A., Merrick J.M.,
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Saudek D.M., Brandon R.C.
Geoghagen N.S.M.,
aser C.M., Smith H.O.,
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P35206;
                                                                                                                                                                                                                                                                                                                              chromosome II from Saccharomyces cerevisiae reveals 16 open reading frames, including ten new open reading frames, five previously identified genes and a homologue of the SCO1 gene.";
Yeast 10:S75-S80(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CSG2 protein precursor.
CSG2 OR CLS2 OR YBR03SC OR YBR0404.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fung1; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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01-FEB-1994 (Rel. 28, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
CSG2 protein precursor.
  the
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                                                                                                                                                                                                                                 Schulze M., Roedel G.;
"Accumulation of the cytochrome c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95157516; pubMed=7854312;
Takita Y., Ohya Y., Anraku Y.;
Takita Y., Ohya Y., Anraku Y.;
"The CLS2 gene encodes a protein with multiple membrane-spanning domains that is important Ca2+ tolerance in yeast.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94171742; PubMed
Beeler T.J., Gable K., Z.
"A novel protein, CSG2p,
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                                                                                                                                                                                           nuclear SCO1 gene.";
                                                                                                                                                                                                               requires a mitochondrial membrane-associated
                                                                                                                                                                                                                                                                           MEDLINE=89281488; PubMed=2543907;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Smits P.H.M.,
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                                                                              Gen. Genet. 216:37-43(1989).

FUNCTION: REQUIRED FOR CALCIUM REGULATION. MAY REACCUMULATION BY A NON-VACUOLE ORGANELLE.

SUBCELLULAR LOCATION: Integral membrane protein.
                      European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WLYWL 151
                                   SWISS-PROT entry is copyright. It is produced through a collaboration the Swiss Institute of Bioinformatics and the EMBL outstation in the Swiss Institute of Bioinformatics and the EMBL outstation in the Swiss Institute of Bioinformatics and the EMBL outstation in the Swiss Institute of Bioinformatics and the EMBL outstation in the Swiss Institute of Bioinformatics and the EMBL outstation in the Swiss Institute of Bioinformatics and the EMBL outstation in the Swiss Institute of Bioinformatics and the EMBL outstation in the Swiss Institute of Bioinformatics and the EMBL outstation in the Swiss Institute of Bioinformatics and the EMBL outstation in the Swiss Institute of Bioinformatics and the EMBL outstation in the Swiss Institute of Bioinformatics and the EMBL outstation in the Swiss Institute of Bioinformatics and the EMBL outstation in the Swiss Institute of Bioinformatics and the EMBL outstation in the Swiss Institute of Bioinformatics and the EMBL outstation in the Swiss Institute of Bioinformatics and the EMBL outstation in the Swiss Institute of Bioinformatics and the EMBL outstation in the Swiss Institute of Bioinformatics and the EMBL outstation in the Swiss Institute of Bioinformatics and the Bioinformatics and 
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4; Conservative
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288
338
360
                      Bioinformatics Institute.
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Gable K., Zhao C., Dunn
ein, CSG2p, is required
cerevisiae.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed-8091864;
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Pred. No. 51;
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Best Local S
Matches 4
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MMUP_ECOLI
Q47689;
Q1-NOV-1997
SEQUENCE FROM N.A.
STRAIN=K12 / W3110;
Takemoto K., Mori H.
Yamamoto Y., Inokuch
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CARBOHYD
CARBOHYD
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DOMAIN
                                                              Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose Mau B., Shao Y.;
                                                                                             SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
STRAIN-812 / MG1655;
MEDLINE-97426617; Pubmed-9278503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D28120; BAA05666.1; -. EMBL; L24113; AAA34533.1; -. EMBL; Z35905; CAA84978.1; -. EMBL; X17441; CAA35491.1; -.
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PROSITE; PS00018; EF_HAND; UNKNOWN_1.
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                                              Science
                                                                                                                                                      Bacteria; Proteobacteria;
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                                                       The
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                                            complete genome sequence of nce 277:1453-1474(1997).
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A53392; A53392.
S41796; S41796.
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2001 (Rel. 40, Last se
2001 (Rel. 40, Last ar
e S-methylmethionine p
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386
 Mori H.,
Inokuchi
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 Murayama
H., Miki
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                                                                                                                                                                                                                                                                                                                                               MW;
                                                                                                                                                      gamma subdivision; Enterobacteriaceae;
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Pred.
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EF-HAND (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL)

N-LINKED (GLCNAC. . .) (POTENTIAL)

W -> L (IN REF. 2 AND 3).

84331D80202CB19C CRC64;
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Z F
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                                                     Escherichia coli K-12.";
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No. 58;
 Kataoka
Hatada I
                                                                                                                                                                                                  update)
                                                                                                                                                                                                                             467
                                                                                                                                                                                         update)
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(See http://www.isb-sib.ch/announce/
a K.,
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, Yano M., I
Fukuda R.,
                                                                                                                                                                                                                                                                                                                           Length 410;
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                                                                        Rose D.J.,
                                                                              Burland V.
          Itoh
  Ichihara
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RESULT 15
ROCE_BACSU
ID ROCE_B
AC P39137
DT 01-FEB
DT 15-JUN
DE Amino-
GN ROCE.
OS Bacill
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Best Local S
Matches 4
                        ROCE_BACSU STANDARD; PRT; 467 AA p39137; 01-FEB-1995 (Rel. 31, Created) 01-FEB-1995 (Rel. 31, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no westure by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-services.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "S-methylmethionine metabolism in Escherichia coli.";
J. Bacteriol. 181:662-665(1999).
-i- FUNCTION: TRANSPORTER FOR THE INTAKE OF S-METHYLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Davis
                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (s or send an email to license@isb-sib.ch).
  Bacillus subtilis
                  Amino-acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Systematic sequencing of the Escherichia coli genome: analysis of the 4.0 - 6.0 min (189,987 - 281,416bp) region."; Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mizuno T., Makino K., Nakata A., Yura T., Sampei G., Mizobuchi K.;
                                                                                                                                                                                                                                                                                                                            InterPro;
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D83536; BAA77928.1; ALT_INIT.
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., Federspiel N., Hyman R., Kalman S.
i D., Lew H., Lin D., Namath A., Oefr
                                                                                                                                            Similarity
4; Conser
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; IPR002293; AA/rel_prmeasel.

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., Komp C., Kurdi O.,
ner P., Roberts D.,
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                                                                                                                                             Indels
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                InterPro;
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RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
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RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Fabret C., Ferrari E., Foulger D.,
RA Choi S.K., Codani J.J., Fabret C., Ferrari E., Foulger D.,
RA Choi S.K., Codani J.J., Haga K., Furna S., Galizzi A., Galleron N.,
RA Glim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Presecan E., Pujic P., Purnelle B., Rapport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
RA Persecan E., Pujic P., Purnelle B., Rapes M., Sadale F.,
RA Seto T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Sekliguchi A., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Vlari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
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                                                                                                           EMBL; D81802; CAAF7399.1; -.
EMBL; D78193; BAA11292.1; -.
EMBL; Z99124; CBAB16070.1; -.
Subtilist; BG10933; roce.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the El
European Bioinformatics Institute. There are no rest:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEGRADATIVE PATHWAY. PROBABLY TRANSPORTS ARGININE OR SUBCELLULAR LOCATION: Integral membrane protein.
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IPR002293; AA/rel_prmease1
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                                                                                                                                                                                                                                                                                                    equires a license agreement (See http://www.isb-sib.ch/announce/email to license@isb-sib.ch).
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DR Pfam; PF00324; aa_permeases; 1.

RP ROSITE; PS00218; AMINO_ACID_PERMEASE_1; 1.

KW Transport; Amino-acid transport; Transmembrane; Complete proteome. FT TRANSMEM 21 41 POTENTIAL.

FT TRANSMEM 47 67 POTENTIAL.

FT TRANSMEM 122 142 POTENTIAL.

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FT TRANSMEM 246 266 POTENTIAL.

FT TRANSMEM 246 266 POTENTIAL.

FT TRANSMEM 336 356 POTENTIAL.

FT TRANSMEM 336 356 POTENTIAL.

FT TRANSMEM 361 381 POTENTIAL.

FT TRANSMEM 409 429 POTENTIAL.

FT TRANSMEM 435 455 POTENTIAL.

SQ SQUENCE 467 AA; 51634 WW; B1A522C03134E6C2 CRC64;

Query Match 235 Score 35; DB 1; Length 467;

Best Local Similarity 80.0%; Pred. No. 65;

Vatches 4; Conservative 1; Mismatches 0; Gaps 0;

1 WLYWI 5

1 WLYWI 102

Search completed: January 3, 2003, 15:29:20

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Sp_archea:*

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         29neq0 caenorhabdi
296tz3 neurospora
001260 caenorhabdi
098gk3 rhizobium 1
064622 rattus norv
091ba4 potamotrygo
099m14 mus musculu
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014562 homo sapien
09xw49 caenorhabdi
08xzu8 ralstonia s
09v596 drosophila
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Q21056 caenorhabdi
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Q8xtj4 ralstonia	Q8z962 salmonella		Q99qq8 streptomyce	Q35341 podospora a	Q12302 saccharomyc	Q92dy2 listeria in	Q8yy42 anabaena sp	Q9ktf6 vibrio chol	042765 candida alb	Q8y9s1 listeria mo	Q9fzr2 mycoplasma	Q9ryt4 deinococcus	Q8x9s3 escherichia	Q9h4j9 homo sapien	Q9cjk5 pasteurella	Q8q1f7 mamestra o	Q8wn96 bos taurus	088572 mus musculu		Q8st66 dictyosteli	a	Q9hkv9 thermoplasm	074899 schizosacch	O)		Q96xr2 sulfolobus		Q922e7 mus musculu

## ALIGNMENTS

RESULT 1 018667 018667 PRELIMINARY; PRT; 3944 AA. AC 018667; DT 01-NOV-1996 (TIEMBLIFE1. 01, Created) DT 01-NOV-1996 (TIEMBLIFE1. 05, Last sequence update) DT 01-DEC-2001 (TIEMBLIFE1. 05, Last sequence update) DT 01-DEC-2001 (TIEMBLIFE1. 19, Last annotation update) DE (47D12.1, protein.  GN C47D12.1, protein.  GN Cachard AA.  AA.  RA Galadsty S.;  RN [1]  RN [1]  RN [1]  RN [1]  RN [1]  GN ADDITIONAL AA.  RN [2]  GN ADDITIONAL AA.  RN [2]  R
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A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Kadota K., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Salto R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Frunno M., Aono H., Baldareili R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzareili J., Mombaerts P.,
RA Mordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Rasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Waltz C., Whittaker C., Wilming L.,
Havashiyaki Y., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Best Local
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Submitted (JUL-2001) to the EMBL,
EMBL; AK011862; BAB27886.1; -.
EMBL; BC011313; AAH11313.1; -.
MGD; MGI:107301; D7Wsu128e.
InterPro; IPR000626; Ubiquitin.
Pfam; P800240; ubiquitin; 1.
SMART; SM00213; UBG; 1.
014562;
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01-JAN-1998
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DNA segment, Chr 7, Wayne state University 128, expressed (Unknown)
(Protein for MGC:19443).
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STRAIN-057BL/6J; TISSUE-EMBRYO;
MEDLINE-21085660; Pubmed-11217851;
                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wynshaw-Boris A
Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D7WSU128E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9D029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3252 WLYWLP 3257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                          286
                                                                                                       w
                                                                                                                                                                                                                                          Local
                                                                                                                                                                                          1 WLYWIP 6
                                                                                                                                                          AAMAAM
                                                                                                                                                                                                                          Similarity
4; Conserv
                                                                                                                                                                                                                                                                                                            PS00299; UBIQUITIN_1; UNKNOWN_1. PS50053; UBIQUITIN_2; 1.
                                                                                                                                                          291
                 (TrEMBLrel.
                                                                                                                                                                                                                            Conservative
                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                              Α.
                                                                                                                                                                                                                                                                                              33449 MW;
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                05,
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    Last sequence update)

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Sciurognathi; Muridae;
                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                          9063F4CB4E5A9C8E CRC64;
                                                                       533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         309
                                                                                                                                                                                                                                            DB
53;
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; Murinae; Mus
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QΥ

MLYWIP

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Q9XW49
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Best Local S
Matches 4
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Q9XW49;
Q9XW49;
01-NOV-1999 (TrEMBLrel. 1:
01-NOV-1999 (TrEMBLrel. 1:
01-MAR-2002 (TrEMBLrel. 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SMUVELL,
PROSITE; PS00299; UBIQUITIN_1,
PROSITE; PS50053; UBIQUITIN_2;
PROSITE; PS50053; UBIQUITIN_1,
PROSITE; PS50053; UBIQUITIN_2;
                                                                                                                                                                                                        investigating biology.";
Science 282:2012-2018(1998).
EMBL; AL033536; CAA22142.1; -.
InterPro; IPR003439; ABC_transportr.
InterPro; IPR001623; DnaJ_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99425270; PubMed=10493829;
Loftus B.J., Kim U.J., Sneddon V.P., Kalush F., Brandon R., Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L., Deslattes Mays A., Cao Y., Xu R.X., Kang H.L., Mitchell S., Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;
"Genome duplications and other features in 12 Mb of DNA sequent of the sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Nemata
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00240; ubiquitin; 1. SMART; SM00213; UBQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                         PRODOM; PD000006; ABC_transportr; 2.
PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_2.
PROSITE; PS00636; DNAJ_1; UNKNOWN_1.
SEQUENCE 1564 AA; 176701 MW; DC66A3E7ED8D
                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (NOV-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           White S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Y53C10A.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y53C10A.9 protein.
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                                                                                                                                                                                     Pfam; PF00005; ABC_tran; 2
                                                                                                                                                                                                                                                                                                                "Genome sequence of the nematode
                                                                                                                                                                                                                                                                                                                                                     none;
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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  Similarity 4; Conserv
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4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR000626; Ubiquitin.
    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nematoda; Chromadorea; Rhabditida; Rhabditoidea; rinae; Caenorhabditis.
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                        88.6%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 to the EMBL/GenBank/DDBJ databases
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12,
20,
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                        Score 39; I
Pred. No. 3.
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  Mismatches
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                                                                                         DC66A3E7ED8DC50F CRC64;
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                                                DB 5;
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                        .3e+02;
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                                           Length 1564;
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
An Ananatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
An Ananatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,
An George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
An Evandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Barandon R.C., Batter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
An Harin J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basun A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Chamber B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkev B.C., Dunn P.,
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N. Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.;
                                                                                                                                                                                                                                             MEDLINE-20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                 STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                CG12929 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ralstonia solanacearum (Pseudomonas solanacearum). Bacteria; Proteobacteria; beta subdivision; Ralsto
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01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                NCBI\_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence of the plant pathogen Ralstonia solanacearum.";
Nature 415:497-502(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 WLFWLP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 WLYWIP 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8263 MW;
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13,
17,
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Last annotation updat
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Pred. No.
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RESULT 7

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A Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
A Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
A Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
A Reinert K., Reminqton K., Sannders R.D.C., Scheeler F., Shen H.,
A Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
A Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
A Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
A Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
A Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,

"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
                                                                              Matches
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ŚTRAIN-ATCC 15692 / PAO1;

MEDLINE=20437337; PubMed=10984043;

MEDLINE=20437337; PubMed=10984043;

Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener Stover C.K., Pham X.-O.T., Erwin A.L., Westbrock Fooding S., Yuan Garber R.L., Goltry L., Tolentino E., Westbrock Fooding S., Yuan Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R. Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an Opportunistic pathogen.";

Nature 406.959-964(2000).
                                                                                                                                                                                                                           EMBL; AE004654; AAG05675.1; -. Hypothetical protein; Complete SEQUENCE 211 AA; 23043 MW;
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01-NOV-1996
01-JUN-2002
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SPYCHALLA J.P., Browse J.;
SPYCHALLA J.P., Browse J.;
"The fat-1 gene of Caenorhabditis elegans
"The fat-1" gene of Caenorhabditis elegans
"The FMBL/GenBank/"
                                             Submitted (OCT-2001) to the EMBL/GenBank/DDBJ EMBL; AL132901; CAB60965.1; -.
EMBL; AL132951; CAC44309.1; -.
InterPro; IPR001225; FA_desaturase.
Pfam; PF00487; FA_desaturase; 1.
                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Y67H2B.a protein (Y67H2A.8 protein).
Y67H2B.A OR Y67H2A.8.
                          SEQUENCE
                                   ProDom;
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Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases
EMBL; L41807; AAA67369.1; -.
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Science 282:2012-2018(1998).
                                                                                                                                                                   none;
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ProDom; PD001081; FA_desaturase;
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Matches 4; Conservative
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01-JUL-1997 (TrEMBLrel. 0
01-JUL-1997 (TrEMBLrel. 0
01-DEC-2001 (TrEMBLrel. 1
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01-DEC-2001 (TrEMBLrel. 19, Crea
01-DEC-2001 (TrEMBLrel. 19, Last
01-MAR-2002 (TrEMBLrel. 20, Last
Hypothetical 62.9 kDa protein.
B9B15.005.
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                                                            Submitted (DEC-1995)
                                                                                SEQUENCE FROM N.A.
                                                                                                            Eukaryota; Metazoa; Nemata
Rhabditidae; Peloderinae;
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Pfam; PF00172; Zn_clus; 1.
PROSITE; PS00463; ZN2_CY6_FUNGAL_1;
PROSITE; PS50048; ZN2_CY6_FUNGAL_2;
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
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                    none;
                                                                       Lloyd C.R
                                                                                                  NCBI_TaxID=6239;
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"Genome sequence of the nematode investigating biology.";
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Nyakatura G., Mewes
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66.7%;
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         C.elegans:
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                                                                                                                                                                                                                                                                                            0;
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RESULT 13
Q6462
ID Q6462
AC Q6462
DT 01-NO
DT 01-DE
DE Prote
GN PTP-S
OS Rattu
OC Eukar
OC Mamma
OX NCBI.
RN [1]
RP SEQUE
RC STRAI
RX MEDLI
RA Reddy
RT trans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
Q98GK3
                                                                                                                                                                                                                                                                                                                                                                                                      DT AC
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Best Local
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Best Local
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                                                                                                                                                                      Q64622;
Q64622;
Q1-NOV-1996
Q1-NOV-1996
Q1-DEC-2001
                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Protein-tyrosine-phosphatase (EC 3.1.3.48) (Fragme PTP-S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q98GK3;
                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001880; MSion_channel pfam; PF00924; MS_channel; I. Hypothetical protein; Complete proi SEQUENCE 739 AA; 81423 MW; E570
                          STRAIN-SPRAGUE-DAWLEY;
MEDLINE-96125184; PubMed-8534367;
Reddy R.S., Swarup G.;
                                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasa Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimot Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the nitrogen-fixing symbioti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation updat
Hypothetical protein ml13287.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 282:2012-2018(1998).
EMBL; Z68220; CAA92491.1; -.
SEQUENCE 739 AA; 85116 MW;
transmembrane protein
               "Alternative splicing
                                                                  SEQUENCE FROM N.A
                                                                                NCBI_TaxID=10116;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete genome structure Mesorhizobium loti.";
DNA Res. 7:331-338(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21082930; PubMed=11214968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-MAFF303099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bactería; Proteobactería; alpha subdivision; Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rhizobium loti (Mesorhizobium loti)
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                                                                                                                                                                                                                                                                                             259 WFYWLP
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                                                                                                                                                                                                                                                                                                                       1 WLYWIP
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5; Conserv
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                                                                                                                                                                                                                                                                                              264
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83.3%;
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generates four different for tyrosine phosphatase mRNA.";
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Pred. No. 2.4e
1; Mismatches
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                                                                                                      Craniata; Vert
Sciurognathi;
                                                                                                                                                                                                                            PRT;
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E57C8EEB5A704087 CRC64;
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             different forms
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                                                                                                       Vertebrata;
thi; Muridae;
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                                                                                                                                                          n update)
(Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             symbiotic bacterium
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                                                                                                       Euteleostomi;
; Murinae; Rat
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               0f
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Q99M14
ID Q99M1
ID Q99M1
AC Q99M1
DT 01-JU
DT 01-JU
DT 01-MA
DE Cathe
GN CTSS.
OS Mus m
OC Mamma
OX NCBI_
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Q9IBA4
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Best Local S
Matches 5
                                         Q99M14;
Q1-JUN-2001 (TrEMBLrel. 1-
01-JUN-2001 (TrEMBLrel. 1-
01-MAR-2002 (TrEMBLrel. 2-
7-+hepsin S.
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Best Local
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=20219325; PubMed=10754074;
Ono-Koyanagi K., Suga H., Katoh K., Miyata T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9IBA4;
01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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                                                                                                                    Q99M14
                                                                                                                                                                                                                                                                                                            PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP;
                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00102; Y_phosphatase; 1. PRINTS; PR00700; PRTYPHPHTASE. SMART; SM00194; PTPC; 1.
                                                                                                                                                                                                                                                                                                                                                                                               J. MOL. EVOL. 50:302-311(2000).
EMBL; AB033582; BAA95189.1; -.
HSSP; P18031; 1BzJ.
InterPro; IPR000387; TYR_phosphatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Potamotrygon motoro (South American freshwater stingray).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii, Squalea; Hypnosqualea; Pristiorajea; Batoidea;
Myllobatiformes; Myliobatoidei; Potamotrygonidae; Potamotrygon.
           Eukaryota; Metazoa; Mammalia; Eutheria;
                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                 vertebrates.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RYPTPN3.
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                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000242; Tyr_PP
                                                                                                                                                                               293 WLYWKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Conserv
                                                                                                                                                                                                                             Similarity 5; Conser
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                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                             Conservative
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8194 MW;
           Chordata;
Rodentia;
                                                                                                                                                                                                                                                                             36954 MW;
                                                                                                                                                                                                                                       84.1%;
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83.3%;
                                                                      17,
17,
20,
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                                                                   Last sequence update)
Last annotation updat
                                                                                              Created)
                                                                                                                                                                                                                                       Score 37;
Pred. No.
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Pred. No.
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        Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                             B0045D23E66F1197 CRC64;
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39;
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           Muridae;
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the early evo
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                      Euteleostomi;
           Murinae;
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RR SEQUENCE FROM N.A.

Straubberg R.: 2001) to the EMBL/GenBank/DDBJ databascs.

RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databascs.

RL Submitted
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Run

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB
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and is derived
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     of hits satisfying chosen parameters:
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1: /cgn2_6/ptodata/1.
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3: /cgn2_6/ptodata/1.
4: /cgn2_6/ptodata/1.
5: /cgn2_6/ptodata/1.
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length: 2000000000
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Gapop 10.0 ,
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     WLYWIP 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
   GenCore version (c) 1993 - 2003
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US-09-330-235-2
US-08-356-5971-159
US-08-190-788A-233
US-08-465-391A-233
US-08-465-391A-233
US-08-465-391A-233
US-08-465-391A-233
US-08-465-391A-233
US-08-463-0762-287
US-09-372-422A-28
US-09-372-422A-28
US-08-91-677-4
US-08-91-677-4
US-08-311-363-15
US-08-311-363-15
US-08-131-363-13
US-08-131-363-13
US-08-131-363-13
US-08-131-163-10
US-08-149-097D-36
US-08-223-305C-47
US-08-223-305C-47
US-08-223-305C-47
US-08-223-305C-47
US-08-223-305C-47
US-08-223-305C-47
US-08-223-305C-47
US-09-268-163-6
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(without alignments)
19.615 Million cell updates/sec
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2, Appli
159, App
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287, Appl
26, Appli
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113, Appli
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114, Appli
115, Appli
116, Appli
117, Appli
118, Appli
119, 
Appli
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Qy
                                 Matches
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Query Matc Best Local Matches	RESULT 1  Sequence 2, Applicant info GENERAL INFO ADDRESSES STREET: STREET: STREET: COUNTRY: COMPUTER RI MEDIUM TY COMPUTER RI MEDIUM TELLEPHONI REFERENCI TELEPHONI TOPOLOGY: US-09-025-578-2	44444000000000000000000000000000000000
h 86.4%; Score 38; DB 4; Len Similarity 66.7%; Pred. No. 65; 4; Conservative 1; Mismatches 1;	RESULT 1  US-09-025-578-2  US-09-025-578-2  Sequence 2, Application US/09025578  Patent No. 6194167  GENERAL INFORMATION: APPLICANT: John A. Browse and James P. Spychalla TITLE OF INVENTION: OMEGA-3 FATTY ACID DESATURASE NUMBER OF SEQUENCES: 2  CORRESPONDENCE ADDRESS: ADDRESSEE: Alan E. Dow, Ph.D. STREET: One World Trade Center STREET: Sulte 1600  CITY: Portland STATE: Oregon COUNTRY: United States of America ZIP: 97204  COMPUTER READABLE FORM: MEDIUM TYPE: Disk, 3-1/2 inch COMPUTER: LIBM PC compatible OPERATING SYSTEM: MS DOS SOFTWARE: WordPortect 5.1  CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/025,578  FILING DATE: Herewith CLASSIFICATION UNMBER: US/09/025,578  FILING DATE: February 18, 1997 CLASSIFICATION UNMBER: 35,123  REFERENCE/DOCKET NUMBER: 4630-49462/AED FREDOMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 402 amino acid residues TYPE: amino acid STRANDEDNESS: Single stranded TOPOLOGY: linear  US-09-025-578-2	33 75.0 118 4 US-09-134-001C-4174 33 75.0 247 4 US-09-372-422A-48 33 75.0 249 4 US-09-372-422A-30 33 75.0 249 4 US-09-372-422A-30 33 75.0 249 4 US-09-372-422A-30 33 75.0 250 4 US-09-372-422A-34 33 75.0 254 4 US-09-372-422A-34 33 75.0 254 4 US-09-372-422A-34 33 75.0 608 4 US-09-372-422A-34 33 75.0 608 4 US-09-372-422A-34 33 75.0 674 1 US-08-864-785-1 33 75.0 674 1 US-08-803-973-7 33 75.0 707 1 US-08-803-973-1 33 75.0 746 1 US-08-803-973-1 33 75.0 746 5 PCT-US95-09323-11 33 75.0 777 5 PCT-US95-09323-2 34 75.0 777 5 PCT-US95-09323-2
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Gaps		4174, Ap 8, Appli 48, Appli 22, Appli 6, Appli 6, Appli 11, Appli 7, Appli 7, Appli 12, Appli 13, Appli 14, Appli 17, Appli 18, Appli 19, Appli 11, Appli 11, Appli 11, Appli 12, Appli 13, Appli 14, Appli 15, Appli 16, Appli 17, Appli 18, Appli 19, Appli 11, Appli 11, Appli 12, Appli 12, Appli 13, Appli 14, Appli 15, Appli 16, Appli 17, Appli 18, Appli 19, Appli 10, Appli 11, Appli 11, Appli 12, Appli 13, Appli 14, Appli 15, Appli 16, Appli 17, Appli 18, Appli 19, Appli 10, Appli 11, Appli 11, Appli 12, Appli 12, Appli 13, Appli 14, Appli 15, Appli 16, Appli 17, Appli 18, Appli 19, Appli 11, Appli 11, Appli 12, Appli 12, Appli 13, Appli 14, Appli 15, Appli 16, Appli 17, Appli 17, Appli 18, Appli 19, Appli 11, Appli 20, Appli 21, Appli 22, Appli 23, Appli 24, Appli 25, Appli 26, Appli 27, Appli
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261 WYYWVP 266

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RESULT 3
US-08-556-597-159
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ORGANIZM: Caenorhabditis elegans
US-09-330-235-2
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APPLICANT: KNUTZON, Debbie
TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN PLANTS
FILE REFERENCE: MOCO.156.00US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 159, Application US/08556597 Patent No. 5877155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn version 3.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09330235 Patent No. 6459018
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CURRENT FILING DATE: 1999-06-10
PRIOR APPLICATION NUMBER: 60/089,043
PRIOR FILING DATE: 1998-06-12
NUMBER OF SEQ ID NOS: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                     TELEFAX: (716) 263-1600 INFORMATION FOR SEQ ID NO:
                   SEQUENCE CHARACTERISTICS:
                                                                    NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 208
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1636
                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 17-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN ID/IX NUMBER OF SEQUENCES: 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Miller, APPLICANT: Lyle, V:
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              261 WYYWVP 266
                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                               FILING DATE: CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
 LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Nixon, Hargrave, Devans & Doyle LLP Clinton Square, P.O. Box 1051
10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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                                        159:
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Pred. No.
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65;
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: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
US-08-556-597-159
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US-08-190-788A-233
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                                                      Matches
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                                                                                  Query Match
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Matches 3; Conserv
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                                                                                                                                                                                                                                                                                                                     EILING DALL:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/'
APPLICATION NUMBER: US 07/'
TO DATE: 05-MAR-1992
                                                                                                                                                                                                                                          FILING DATE: 05-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REFERENCE/DOCKET NUMBER: 1019
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-496-2300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,788 FILING DATE: 02-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Peptides and Compounds That Bind to TITLE OF INVENTION: IL-1 Receptor NUMBER OF SEQUENCES: 312
CORRESPONDENCE ADDRESS:
                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                      Local Similarity 66. les 4; Conservative
                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 4001 Min
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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                                                                                                                                           TOPOLOGY:
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                         1 WLYWIP 6
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                                                                                                                                                                                                                                 415-424-0832
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Baldwin, David N.
Jacobs, Jeff W.
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                                                                                                                                           linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
                                                                                                                           peptide
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                                                                                                                                                      single
                                                                   77.3%;
66.7%;
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                                                                     Score 34;
Pred. No.
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Pred. No.
                                                      Mismatches
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                                                                   DB 1;
13;
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                                                      Indels
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RESULT 5 US-08-383-474B-236 ; Sequence 236, Application US/08383474B

GENERAL INFORMATION:

Barrett, Ronald

Yanofsky,

Stephen

5767234

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RESULT 6
US-08-465-391A-233
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APPLICANT: Barret
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NUMBER OF SEQUENCES: 314
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
Townsend & Townsend & Crew LLP
Townsend & Townsend & Crew LLP
        CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 415-496-2300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,788
FILING DATE: 02-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                  APPLICANT:
                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Baldwin, David N. APPLICANT: Jacobs, Jeff W. TITLE OF INVENTION: Peptides TITLE OF INVENTION: the IL-1
                                                                                    TITLE OF INVENTION:
                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                   APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 01-FEH
                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 66. es 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Stevens, Lauren L
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                       1 WLYWIP 6
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San Francisco
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Jacobs, Jeff W.
Bovy, Phillipe R.
Leahy, Ellen M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             California
                                                                                                                Pottorf, Richard S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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                                                                                                                                                                                                                      Barrett, Ronald W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ss: single
linear
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                                                                             Peptides and Compounds That Bind to IL-1 Receptor
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66.7%;
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Pred. No.
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US-08-464-538B-233
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                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 233, Application US/08464538B Patent No. 5861476
                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                STREET: Two LINE CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: NO. 5786331viel, V
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 01-FEB-1995
                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 02-FEB-1994
                                                                                                                                                                                                                   APPLICANT: Pottorf, Richard S.
TITLE OF INVENTION: Peptides and Compounds That Bind
TITLE OF INVENTION: IL-1 Receptor
NUMBER OF SEQUENCES: 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version.#1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 05-JUI
                                                                                                  COUNTRY: UZIP: 94111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: California
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                                                                                                                                                                                                                                                                                                      Jacobs, Jeff W.
Bovy, Phillipe R.
                                                                                                                                                                                                                                                                                                                                      Baldwin,
                                                                                                                                                                                                                                                                                        Leahy, Ellen M.
                                                                                                                                                                                                                                                                                                                      Yanofsky, Stephen D.
Baldwin, David
Jacobs, Jeff W.
                                                                                                                                                                                                                                                                                                                                                                           Barrett, Ronald W
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66.7%;
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32,483
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APPLICATION NUMBER: FILING DATE: 05-JUI

05-JUN-1995

US/08/464,538B

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; MOLECULE TYPE:
US-08-464-538B-233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION UNBER: 30,223
REFERENCE/DOCKET NUMBER: 1652
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                              TELEFAX: (415) 576-03
                                                                                                                                                                CLASSIFICATION: 514 ATTORNEY/AGENT INFORMATION: NAME: Snyder, Joseph R
                                                                                                                                                                                                                                                                         ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Barrett, Ronald W.
APPLICANT: Yanofsky, Stephen D.
TITLE OF INVENTION: Peptides and Compounds That Bind
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid•
                                                                  NAME: Snyder, Joseph R.
REGISTRATION NUMBER: 39,381
REFERENCE/DOCKET NUMBER: 16528A-001850US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 01-FEB-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,788
FILING DATE: 02-FEB-1994
                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 392
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/373,474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                           APPLICATION NUMBER: US/08/463,076E FILING DATE: 05-JUN-1995 CLASSIFICATION: 514 .
                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 01-FE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 WLYWIP 6
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5. 5880096
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Pred. No.
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Вp
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                                                                                                                                                SEQ ID NO 26
LENGTH: 272
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 28
LENGTH: 257
TYPE: PRT
                                                          Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                        Sequence 26, Application US/09372422A
Patent No. 6313375
                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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Best Local Similarity
                                                                                     Query Match
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                                                                                                                                                                                                       FILE REFERENCE: 0919
CURRENT APPLICATION NUMBER: US/09/372,422A
CURRENT FILING DATE: 1999-08-11
PRIOR APPLICATION NUMBER: US 60/098,692
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 49
                                                                                                                                                                                                                                                                                             APPLICANT: Rudolf Jung
APPLICANT: Francois Barrieu
TITLE OF INVENTION: Maize Aquaporins and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/372,422A CURRENT FILING DATE: 1999-08-11 PRIOR APPLICATION NUMBER: US 60/098,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Rudolf Jung
APPLICANT: François Barrieu
TITLE OF INVENTION: Maize Aquaporins and Uses Thereof
FILE REFERENCE: 0919
                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                   ORGANISM: Zea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Zea
                                                                                                                                                                                                                                                                                                                                                                                                                                                   222 WVYWI 226
220 WVYWI 224
                                                       Local Similarity les 4; Conserv
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4 WYYWQP 9
                             1 WLYWI 5
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                                                          Conservative
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80.0%;
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66.78;
                                                                        77.3%;
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Pred. No. 13;
1; Mismatches
                                                         Score 34; DB 4;
Pred. No. 1.8e+0
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 34; DB 4;
Pred. No. 1.7e+02;
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13;
                                                                       1.8e+02;
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RESULT 12
US-07-745-206A-15
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US-07-745-206A-15
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US-08-991-677-4
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APPLICANT: Chiang, Vincent L

APPLICANT: Carraway, Daniel T

APPLICANT: Smeltzer, Richard H

TITLE OF INVENTION: Production of Syringyl Lignin in Gymnosperms

FILE REFERENCE: 50617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15,
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/08/991,677A CURRENT FILING DATE: 1997-12-16 EARLIER APPLICATION NUMBER: US 60/033,381 EARLIER FILING DATE: 1996-12-16 NUMBER OF SEQ. ID NOS: 11
                                                                                            ATTORNEY/AGENT INFORMATION:

NAME: Feder, Scott B
REFERENCE/DOCKET NUMBER: 5150
TELECHMUNICATION INFORMATION:
TELEPHONE: 312-372-7842
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Liquidambar styraciflua 08-991-677-4
                                                         INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 823 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 511
                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/745,206A
FILING DATE: 19910815
              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Feldman, Daniel TITLE OF INVENTION: Human CONTITLE OF INVENTION: Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            224 WLKWVP 229
                                                                                                                                                                                                   FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                           CITY: Chicago
STATE: Illinois
                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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o. 6252135
                                            H: 823 amino acids
AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  McCue, Ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ellis, Steven
Williams, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harpold, Michael
Ellis, Steven
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          protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human Calcium Channel Compositions and
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Pred. No. 3.4e+02;
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RESULT 14
US-07-745-206A-13
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Best Local Similarity
"~+~hes 5; Conserva
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US-08-311-363-15
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                                    Sequence 13, Application US/07745206A Patent No. 5429921
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Best Local Similarity
Matches 5; Conser
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 15,
                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               APPLACATE:
FILING DATE:
PRIOR APPLICATION NUMBER: US
APPLICATION NUMBER: 15-AUG-190
                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                     FILING DATE: 15-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 823 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Ma
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                    333 WLYFIP 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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Harpold, Michael
Ellis, Steven
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VENTION: Human Calcium Channel Compositions and
                                                                                                                                                                                                                                                                                                                        (619)238-0062
                                                                                                                                                                         Conservative
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Feldman, Daniel
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83.3%;
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Pred. No. 5
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Pred. No. 5.3e+02;
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APPLICANT: Williams, Daniel
APPLICANT: Weldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: Human Calcium Channel Compositions and
TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
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US-08-311-363-13
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Matches 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Feder, Scott B
REFERENCE/DOCKET NUMBER: 51:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-372-7842
INFORMATION FOR SEQ ID NO: 13:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1754 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/745,206A
FILING DATE: 19910815
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APPLICANT: McCue, Ann
APPLICANT: Feldman, Daniel
TITLE OF INVENTION: Human Calcium Channel Compositions and
TITLE OF INVENTION: Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitch, Even, Tabin & Flannery
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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333 WLYFIP 338
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hes 5; Conserv
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Ellis, Steven
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83.3%;
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1; Mismatches
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1.1e+03;
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                                                                                                  Matches
                                                                                                                                                                                                                                               TELEFAX: (619)238-006
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1754 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                      NAME: Scidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-51506
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 15-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                        333 WLYFIP 338
                                                                                                 Local Similarity
nes 5; Conserv
                                                                                                                                                                                                                                                                          TELEPHONE:
                                                                    1 WLYWIP 6
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                                                                                                  Conservative
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                                                                                                              77.3%;
83.3%;
3, 2003, 15:34:28
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Pred. No.
                                                                                                  Mismatches
                                                                                                              1.1e+03;
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                                                                                                                          Length 1754;
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Search completed: January Job time : 10 secs

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Minimum DB seq
Maximum DB seq
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 Published_Applications_Aa:*

1: /cgn2_6/ptodata/1/pubpaa/U
2: /cgn2_6/ptodata/1/pubpaa/U
3: /cgn2_6/ptodata/1/pubpaa/U
4: /cgn2_6/ptodata/1/pubpaa/U
6: /cgn2_6/ptodata/1/pubpaa/U
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10: /cgn2_6/ptodata/1/pubpaa/U
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1 WLYWIP 6
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Copyright (c) 1993 - 2003 Compugen Ltd
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10 US-09-815-242-10052
10 US-09-815-242-10052
10 US-09-726-643-8
10 US-09-726-643-39
10 US-09-726-643-39
10 US-09-726-643-39
10 US-09-738-626-4440
10 US-09-738-626-4785
10 US-09-738-626-4785
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12 US-10-033-026-8
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23.825 Million cell updates/sec
           Sequence 58, Appl
Sequence 139, Appl
Sequence 139, App
Sequence 4, Appli
Sequence 4, Appli
Sequence 4785, App
Sequence 4140, Ap
Sequence 10, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 4, Appli
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Sequence 204, Appl
Sequence 204, Appl
Sequence 47931, A
Sequence 11166, A
Sequence 10052, A
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US-10-104-339-2
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169	116	110	79	70	1167	914	777	563	559	519	519	475	475	466	466	463	398	365	288	262	255	221	126	88	56
10	10	10	9	10	10	10	10	10	10	10	9	10	10	10.	10	9	10	10	10	9	10	10	10	10	10
US-09-925-301-902	US-09-741-843-4	US-09-867-550-298	US-09-738-626-4898	US-09-864-761-46021	US-09-815-242-11522	US-09-815-242-10897	US-09-815-242-4894	US-09-915-181A-6	US-09-820-721A-1	US-09-815-242-11388	US-09-895-913A-118	US-09-815-242-11503	US-09-815-242-5055	US-09-815-242-14048	US-09-815-242-10265	US-09-738-626-6946	US-09-729-674-146	US-09-815-242-13185	US-09-925-299-840	US-09-981-353-63	US-09-864-711-15	US-09-925-300-1659	US-09-864-761-48848	-764-853	US-09-864-761-35892
Sequence 902, App	Sequence 4, Appli	Sequence 298, App	Sequence 4898, Ap	Sequence 46021, A	Sequence 11522, A	•	Sequence 4894, Ap	Sequence 6, Appli	Sequence 1, Appli	Sequence 11388, A	Sequence 118, App	11503,	Sequence 5055, Ap	Sequence 14048, A	Sequence 10265, A	Sequence 6946, Ap	Sequence 146, App	Sequence 13185, A	$\sim$	Sequence 63, Appl	15, Ap	Sequence 1659, Ap	Sequence 48848, A		Sequence 35892, A

## ALIGNMENTS

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Sequence 2, Application US/10104339
Patent No. US20020170090A1
GENERAL INFORMATION:
APPLICANT: John A. Browse and James P. Spychalla
TITLE OF INVENTION: OMEGA-3 FATTY ACID DESATURASE
                                                                                           INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                      REFERENCE/DOCKET NUMBER: 4630-49462/AED TELECOMMUNICATION INFORMATION: TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Alan E. Dow, Ph.D.
REGISTRATION NUMBER: 35,123
                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/104,339
FILING DATE: 21-Mar-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSE: Alan E. Dow, Ph.D.
STREET: One World Trade Center
121 S.W. Salmon Street
Suite 1600
                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: MS DOS SOFTWARE: WordPerfect 5.1
                 STRANDEDNESS: single stranded
                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 09/747,755 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Disk,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Portland
STATE: Oregon
                                                               LENGTH: 402 amino acid residues
                                           amino acid
linear
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                                                                                           US-09-801-368-204
                                                                                                                 RESULT 3
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US-09-747-755-2
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                                   Sequence 204, Application US/09801368 Patent No. US20020128250A1 GENERAL INFORMATION:
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Matches
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Patent No. US20020042933A1
GENERAL INFORMATION:
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APPLICANT: Busby, Robert APPLICANT: Cali, Brian
                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Alan E. Dow, Ph.D.
REGISTRATION NUMBER: 35,123
REFERENCE/DOCKET NUMBER: 4630-49462/AED
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Disk, 3-1/2 ind
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Disk, 3
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: John A. Browse and James P. Spychalla TITLE OF INVENTION: OMEGA-3 FATTY ACID DESATURASE
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION NUMBER:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                          261 WYYWVP 266
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                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                             LENGTH: 402 amino acid residues TYPE: amino acid STRANDEDNESS: single stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Alan E. Dow, Ph.D. STREET: One World Trade Center STREET: 121 S.W. Salmon Street STREET: Sulte 1600
CITY: Portland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
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                                                                                                                                                                                                            1 WLYWIP 6
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                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                    Score 38;
Pred. No.
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; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-864-761-47931
           PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Se
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
NUMBER OF SEQ ID NOS: 440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.0 SEQ ID NO 204
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Best Local Similarity
                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR TILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
                                                                                                                                                                                                                        PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: Aeomica-X-1
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Silva, Jeff
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Salama, Sofie
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No. US20020128250Alman,
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Pred. No.
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OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.2
OTHER INFORMATION: EST_HUMAN HIT: BF090287.1, EVALUE 3.10e-01
OTHER INFORMATION: SWISSPROT HIT: P13276, EVALUE 1.90e+00
US-09-864-761-47931
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NUMBER OF SEQ ID NOS: 49117

SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 47931
                                           SEQ ID NO 11186
LENGTH: 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11186, Application US/09815242 Patent No. US20020061569A1
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Best Local
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FITLE OF INVENTION: Identification of Essential Genes
FILE REFERENCE: ELITRA.011A
FILE REFERENCE: ELITRA.011A
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                            PRIOR PRIOR
                                                                                                             PRIOR FILING DATE: 20 NUMBER OF SEQ ID NOS:
                                                                                                                             PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
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PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
                                                                                        SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                              PRIOR
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PRIOR APPLICATION NUMBER: PCT/US01/00662
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TYPE: PRT
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ORGANISM: Haemophilus influenzae
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                                                                                                                                                                        APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
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Zyskind, Judith W.
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Pred. No. 28;
l; Mismatches
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US-10-042-141-58
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                                                                                                                                            Sequence 58, Application US/10042141 Publication No. US20020183503A1 GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10052
LENGTH: 475
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Matches 4; Conserv
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CURRENT APPLICATION NUMBER: US/10/042,141
CURRENT FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: 09/726,643
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US00/15187
                                                                                       APPLICANT: Ruben et al.
TITLE OF INVENTION: 26 Human secreted proteins
FILE REFERENCE: PZ040P1
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PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
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TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
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Yamamoto, Robert T.
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Zyskind, Judith W.
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Pred. No.
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Pred. No. 1
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APPLICANN: Ruben et al.

TITLE OF INVENTION: 26 Human secreted proteins
FILE REFERENCE: PZ040P1
CURRENT APPLICATION NUMBER: US/10/042,141
CURRENT FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: 09/726,643
PRIOR FILING DATE: 2000-12-01
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US00/15187
PRIOR FILING DATE: 2000-06-02
PRIOR FILING DATE: 2000-06-02
PRIOR FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 190
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
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Patent No. US20020028449A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 26 Human secreted proteins
FILE REFERENCE: PZ040P1
CURRENT APPLICATION NUMBER: US/09/726,643
CURRENT FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US00/15187
PRIOR FILING DATE: 2000-06-02
PRIOR FILING DATE: 2000-06-02
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SEQ ID NO 58
LENGTH: 446
TYPE: PRT
ORGANISM: Homo sapiens
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US-10-042-141-58
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Best Local S
Matches 4
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PRIOR APPLICATION NUMBER: 60/137,725
PRIOR FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 190
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 58
LENGTH: 446
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Best Local Similarity
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PRIOR FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 190
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ORGANISM: Homo sapiews
                                                          TYPE: PRT
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                                                                                       ENGTH: 510
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| 141 WVYWI 145
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Local Similarity 80.0%;
les 4; Conservative
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Pred. No. 1.7e+02;
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US-09-796-256A-4
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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LENGTH: 510
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                  224 WLKWVP 229
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                                                                                    1 WLYWIP 6
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Query Match
Best Local Similarity
Tatches 4; Conserve
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                                                                                                                                     SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 511
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09796256A Patent No. US20020078477A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 139, Application US/09726643 Patent No. US20020028449A1
                                                                                                                                                                                                                      APPLICANT: Chiang, Vincent L
APPLICANT: Carraway, Daniel T
APPLICANT: Smeltzer, Richard H
TITLE OF INVENTION: Production of Syringyl Lignin in Gymnosperms
FILE REFERENCE: 50617/c-3532.0
CURRENT APPLICATION NUMBER: US/09/796,256A
CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US60/03381
PRIOR APPLICATION NUMBER: US60/03381
PRIOR FILING DATE: 1996-12-16
PRIOR FILING DATE: 1996-12-16
PRIOR APPLICATION NUMBER: 08/991677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/726,643
CURRENT FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US00/15187
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: 60/137,725
PRIOR FILING DATE: 1999-06-07
                                                                                                                                                                                           PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 11
                                                                                               TYPE: PRT ORGANISM: Liquidambar styraciflua
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                  Conservative
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80.0%;
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80.0%;
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Pred. No. 1.9e
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                                 Score 34; I
Pred. No. 1
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Pred. No. 1.9e+0
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ches 0;
                                 DB 10;
1.9e+02;
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; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4785
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SEQ ID NO 46
LENGTH: 627
TYPE: PRT
ORGANISM: Mus musculus
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Patent No. US20020142428A1
GENERAL INFORMATION:
APPLICANT: Hodge, Martin R.
                                                                                                                                                                                                               SEQ ID NO 4785
                                                                      Matches
                                                                                   Query Match
Best Local Similarity
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Best Local Similarity
Matches 4; Conserva
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                                                                                                                                                                                                                             PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
                                                                                                                                                                                                                                                                                                                                                  APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
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563 WLYWM 567
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OCHIAI, KEIKO
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SENOH, AKIHIRO
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                                                                      Conservative
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80.0%;
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Pred. No. 3.5e+02
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Pred. No. 2.3e+02;
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APPLICANT: OZAKI, AKIO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOSTWARE: PATENTIN VET: 3.0
LENGTH: 1189
TYPEF: PRT
                                                     Query Match
Best Local Similarity
Thehes 5; Conserve
                                                                                                                                             LENGTH: 2237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-033-026-8
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US-10-033-026-8
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US-09-738-626-4140
                                                                                                                                                                                                                       SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/10033026 Patent No. US20020147309A1
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                                                                                                                                                                                                                                                                                     APPLICANT: Lipscombe, Diane
APPLICANT: Schorge, Stephanie
TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF
FILE REFERENCE: B1055/7000
CURRENT APPLICATION NUMBER: US/10/033,026
CURRENT FILING DATE: 2001-12-28
PRIOR APPLICATION NUMBER: US 09/268,163
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: US 60/077,901
PRIOR APPLICATION NUMBER: US 60/077,901
                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1998-03-13 NUMBER OF SEQ ID NOS: 28
                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version
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333 WLYFIP 338
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                                    1 WLYWIP 6
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TATEISHI, NAOKO
SENOH, AKIHIRO
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                                                                        Conservative
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66.7%;
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83.3%;
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Pred. No. 6.7e+02;
1; Mismatches 0;
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Pred. No.
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Search completed: January 3, 2003, 15:52:05 Job time : 5.77273 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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           Issued_Patents_AA:*
1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
6: /cgn2_6/ptodata/1,
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length: 2000000000
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US-08-445-438-7
US-08-447-314-4
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                      Sequence 21, Appl
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Sequence 71, Appl
Patent No. 5179198
Patent No. 5521296
Sequence 17, Appl
Sequence 17, Appl
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                                                                                                                                                         Sequence 15,
Sequence 40,
Sequence 40,
Sequence 18,
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A Sequence 4,
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4275, Ap
4015, Appl
4615, Ap
4298, Ap
18, Appl
3948, Ap
4, Appli
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1 LLLVIA 6

Query Matc Best Local Matches	RESULT 1  US-07-800-364B-15  Sequence 15, Application US/0780036. Patent No. 5686678  GENERAL INFORMATION: APPLICANT: Hewick, Rodney M. APPLICANT: Wanny, Jack H. APPLICANT: Wanny, John M. APPLICANT: Wozney, John M. APPLICANT: Celeste, Anthony J. TITLE OF INVENTION: Bone and Ca. NUMBER OF SEQUENCES: 15 CORRESPONDENCE ADDRESS: ADDRESSEE: Legal Affairs, Gen. STREET: 87 CambridgePark Driv. CITY: Cambridge STATE: MA ZIP: 02140 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-D SOFTWARE: PatentIn Release #1 CURREST APPLICATION UNMBER: US/07/800 FILLING DATE: 26-NOV-1991 CLASSIFICATION UNMBER: US/07/800 FILLING DATE: 26-NOV-1991 CLASSIFICATION INFORMATION: TRELEPHONE: Rapinos, Ellen J. REFERENCE/DOCKET NUMBER: GI 5: TELECHONUBICATION INFORMATION: TELEPHONE: 617-876-5851 INFORMATION FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS: LENGTH: 112 amino acids TYPE: amino acids TYPE: amino acids TYPE: hopology unknown MOLECULE TYPE: peptide HYPOTHETICAL: NO STOLOGY UNKNOWN US-07-800-364B-15		444444 3333333333333333333333333333333
h Simi 6;	1 100-364B-15 00-364B-15 100-364B-15		2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
larity Conserva	*-15 Application US 688678 CORMATION: :: Hewick, Rodn :: Wang, Jack H :: Wozney, John :: Celeste, Ant INVENTION: BON SEQUENCES: 15 DENCE ADDRESS: DENCE ADDRESS: DENCE ADDRESS: Legal Affa AF Cambridge MA  USA USA USA USA USA USA USA USA USA U		
100.0 100.0 ative	ication US/07 ication US/07 ilon: ION: Rodney Wick, Rodney Wick, Rodney John M. Leste, Anthon FIFION: Bone a RATION BLE FORM: Floppy disk		9 5 5 8 2 2 4 4 4 4 4 5 6 6 7 6 6 7 6 7 6 7 6 7 6 7 6 7 6 7 6
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CURRENT APPLICATION NUMBER: US/08/688,988B; CURRENT FILING DATE: 1996-07-31; NUMBER OF SEQ ID NOS: 48 SOFTWARE: FASTSEQ for Windows Version 3.0 EQ ID NO 40 LENGTH: 509
TYPE: PRT ORGANISM: HOrdeum vulgare
US-08-688-988-40
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US-09-134-001C-4615
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Sequence 4615, Application US/09134001C
Patent NO. 6380370
GEMERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCCOCCUS
TITLE OF INVENTION: DIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT, APPLICATION NUMBER: US/09/134,001C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: LYNN DOUCETTE-Stamm et al
APPLICANT: LYNN DOUCETC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TILLE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-108-14
PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lefebvre, Daniel D.
APPLICANT: Malboobl, Mohammad A.
TITLE OF INVENTION: PHOSPHATE STARVATION-INDUCIBLE PROTEINS
FILE REFERENCE: PPL96-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 5674
EQ ID NO 4275
LENGTH: 173
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US-08-740-223A-18
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US-09-134-001C-4298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: LYNN DOUCETTE-Stamm et al
APPLICANT: LYNN DOUCETTE-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: EPIDERWIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                               Sequence 18, Application US/08740223A Patent No. 6265564 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR ETILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4298
LENGTH: 387
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SEQ ID NO 4615
LENGTH: 630
TYPE: PRT
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Best Local Similarity
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PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR EILING DATE: 1997-11-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
                                         ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                    APPLICANT: Davis, et al.
TITLE OF INVENTION: Expressed Ligand - Vascular
TITLE OF INVENTION: Intercellular Signalling Molecule
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 LLLVIA 138
                                                                                                                      CITY: Tarrytown
STATE: NY
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nes 6; Conserv
                                COMPUTER:
                                                                                                                                                         STREET:
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version
                                                                                                        COUNTRY:
                                                                                                                                                       ADDRESSEE: Regeneron Pharmaceuticals, STREET: 777 Old Saw Mill Road
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CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE: 2: CLASSIFICATION:

25-OCT-1996

US/08/740,223A

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RESULT 8
US-09-202-491-4
; Sequence 4, Application US/09202491
; Patent No. 6432667
; GENERAL INFORMATION:
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                                                                                                                                                                        Query Match
Best Local Similarity
Watches 5; Conserva
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Best Local Similarity
"hes 5; Conserva
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT EPILICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064;964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NOS: 5674
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                                                                                                                                                                                                                                                                                               LENGTH: 503
TYPE: PRT
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INFORMATION FOR SEQ ID NO:
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LENGTH: 503 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 02-AUG-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/022/999
FILING DATE: 02-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: FRAGMENT TYPE:
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268 LLLIIA 273
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LOCATION: 1...503
OTHER INFORMATION:
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REGISTRATION NUMBER: 36
REFERENCE/DOCKET NUMBER:
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Pred. No. 9.5e+02;
1; Mismatches C
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Pred. No. 9.5e
1; Mismatches
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9.5e+02;
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RESULT 10
US-09-709-188-18
Sequence 18, Application US/09709188
Patent No. 6441137
GENERAL INFORMATION:
APPLICANT: Davis et al.
TITLE OF INVENTION: Expressed Ligand
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Best Local Similarity
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CURRENT FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: PCT/US97/10728
EARLIER FILING DATE: 1997-06-19
EARLIER APPLICATION NUMBER: 60/022,999
EARLIER FILING DATE: 1996-08-02
EARLIER APPLICATION NUMBER: 60/021,087
EARLIER FILING DATE: 1996-07-02
EARLIER FILING DATE: 1996-07-02
EARLIER APPLICATION NUMBER: 60/021,087
EARLIER FILING DATE: 1996-07-02
EARLIER FILING DATE: 1996-07-02
EARLIER FILING DATE: 1996-06-19
NUMBER: OF SEO ID NOS: 14
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CURRENT APPLICATION NUMBER: US/09/202,491
CURRENT FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: PCT/US97/10728
EARLIER FILING DATE: 1997-66-19
EARLIER APPLICATION NUMBER: 60/022,999
EARLIER FILING DATE: 1996-08-02
EARLIER APPLICATION NUMBER: 60/021,087
EARLIER APPLICATION NUMBER: 60/021,087
EARLIER APPLICATION NUMBER: 08/665,926
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LENGTH: 503
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Best Local :
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NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Valenzuela et al. TITLE OF INVENTION: NOVEL LIGANDS, METHODS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
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12 LLLVVA 17
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Pred. No: 9
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Expressed Ligand - Vascular Intercellular Signaling Molecule 333-Z

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Query Match
Best Local Similarity
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GENERAL INFORMATION:
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Best Local
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                             NAME: HASAK Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 854C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/170558
FILING DATE: 20-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION UMBER: 08/157563
FILING DATE: 23-NOV-1993
ATTORNEY/AGENT INFORMATION:
ADME: 15014
TOCKET
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CURRENT FILING DATE: 2000-11-09
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDLUM TYPE: 5.25 Inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Protein Tyrosine Kinases NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08 FILING DATE: 22-MAY-1995
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STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
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amino acid
GY: linear
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Baron, Will F.
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Mark, Melanie R.
Scadden, David T.
                  Conservative
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             Score 23; DB 1; Le
Pred. No. 1.8e+03;
1; Mismatches 0;
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RESULT 13
US-08-447-314-4
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US-08-170-558-4
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Best Local S
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APPLICANT: Godowsk
APPLICANT: Mark, M
APPLICANT: Scadden
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                                              GENERAL INFORMATION:
APPLICANT: Scadden, David T.
APPLICANT: Baker, Kevin P.
APPLICANT: Baron, Will F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/170,5
FILING DATE: 20-DEC-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/157563
APPLICATION OF 1993
ATTORNEY/AGENT INFORMATION:
NAME: 1504 TO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
CORRESPONDENCE ADDRESS
                              TITLE OF INVENTION: Protein Tyrosine Kinases
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 913 amino acid
                NUMBER OF SEQUENCES:
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TELEY 910/371-7168
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STATE: Callfornia
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TELEFAX: 415/952-9881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
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                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
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Mark, Melanie R.
Scadden, David T.
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Baron, Will F.
                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JMBER: US/08/170,558
20-DEC-1993
                                                                                                                                                                                                                                                                                                           95.8%;
83.3%;
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Pred. No. 1.8e
1; Mismatches
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COUNTRY:

California

1: 460 Point San Bruno Blvd South San Francisco

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Query Match
Best Local Similarity
"hes 5; Conserv?
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-445-461-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEFAX: 415/957-9168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08445461 Patent No. 6096527
                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/170558
FILING DATE: 20-DEC-1993
                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb 1
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                APPLICANT: Baker, Kevin P.
APPLICANT: Baron, Will F.
TITLE OF INVENTION: Protein Tyrosine Kinases
NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PATIN (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/44
FILING DATE: 22-MAY-1995
                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         430 LLLIIA 435
APPLICATION NUMBER: US/01
FILING DATE: 22-MAY-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                           ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
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                                       US/08/445,461
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                                                                                                                               360 Kb floppy disk
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Pred. No. 1.8e+03;
1; Mismatches 0;
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Query Match 95.3
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                 TELEFAX: (212) 869-970
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMÁTION:
NAME: COPUZZÍ, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 766
TELECOMMUNICATION INFORMÁTION:
                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 919 amino acid
                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 08-NOV-199
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ullrich, Axel APPLICANT: Alves, Frauke TITLE OF INVENTION: CCK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 913 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 854
TELECOMMUNICATION INFORMATION:
TELECHONE: 415/225-1896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 20-DEC-PRIOR APPLICATION DATA:
                                                                                LENGTH: 919 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      430 LLLIIA 435
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                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
nes 5; Conserv
                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
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1155 Avenue of the Americas
                                                                                                                                                                                                    (212) 790-9090
(212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                                                                                                                                                                                                          08-NOV-1994
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               95.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A No. 5677144el Receptor Tyrosine Kinase
                                                                                                                                                                                                                                                       7683-065
 Score 23; DB 1;
Pred. No. 1.8e+03;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 23; DB 3;
Pred. No. 1.8e+03;
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                                 Length 919;
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   Indels
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Qy 1 LLLVIA 6
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|| Db 430 LLLIIA 435

Search completed: January 3, 2003, 15:34:29
Job time: 10 secs
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Copyright

GenCore version 5.1.3 (c) 1993 - 2003 Compugen Ltd

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Run
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     al number of hits satisfying chosen parameters:
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                 BLOSUM62
Gapop 10.0 ,
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24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Published_Applications_AA: *
: //cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep: *
    //cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep: *
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    //cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep: *
    //cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep: *
    //cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep: *
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    //cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep: *
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(without alignments)
23.825 Million cell updates/sec
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RESULT 2 US-09-764-853-847    Sequence 847, Application US   Patent NO. US20020090672A1   GENERAL INFORMATION:   APPLICANT: ROSEN et al.   TITLE OF INVENTION: Nucleic   FILE REFERENCE: PUZ06   CURRENT APPLICATION NUMBER   CURRENT FILING DATE: 2001   Prior application data remo	Query Matches  Matches  Qy 1 L Db 10 L	RESULT 1  US-10-016-481-11  US-10-016-481-11  Sequence 11, Application US/10  Patent No. US/20020115610A1  GENERAL INFORMATION:  APPLICANT: Ehlert, Frederick  TITLE OF INVENTION: Prokineti.  TITLE OF INVENTION: Composit  FILE REFERENCE: P-UC 5016  CURRENT APPLICATION NUMBER: UCURENT FILING DATE: 2001-11  PRIOR APPLICATION NUMBER: 60/  PRIOR FILING DATE: 2000-11-03  NUMBER OF SEQ ID NOS: 19  SOFTWARE: FastSEQ for Windows  SEQ ID NO 11  LENGTH: 96  TYPE: PRT  ORGANISM: Bombina variegata  US-10-016-481-11	-	444444933333322222222222 44444493376532110
NO. US2 INFORM INFORM INT: RC FILIN FILIN PFILIN	TTV 111 1 S 1 S	A 481-1. A 10. US. INFORMINT: INF		222222222222222222222222222222222222222
Applica Applica 20020090 MATION: DSEN Et i ENTION: DE: PJZ01 ICATION I ICATION I ICATION I	ilarit Conse 6 15	Application US/10016481 IS20020115610A1 IRMATION: Zhou, Qun-Yong Zhou, Qun-Yong Zhou, Prokineticin Po VENTION: Prokineticin Po VENTION: Compositions a INCE: P-UC 5016 INCE: P		95.8 95.8 95.8 95.8 95.8 95.8 91.7 91.7 91.7 91.7 91.7 91.7 91.7 91.7
tion US/09 672A1 al. Nucleic Ac Nucleic Ac 2001-01-	y 100 y 100 ervative	tion US/1001 5610Al n-Yong Frederick Prokinetic! Compositic C 5016 NUMBER: US/ 1: 2001-11-0 1000BER: 60/20 2000-11-03 or Windows Variegata		326 3177 51394 1210 1210 1069 11067
US/097 Lic Aci Lic Aci R: US/ 11-01-1	000	US/100 Al  ng derick kinetic kinetic generation 100111-103 111-03		10 10 10 10 10 10 10 10 10 10 10
764853 ids, Proteins, and Antik /09/764,853 - consult PALM or file	0; Mismatches 0; Indels	lypeptides, Reland Methods 16,481 2 on 4.0	ALIGNMENTS	US-09-888-615-105 US-10-091-628-2 US-10-091-628-2 US-09-935-301-1388 US-09-935-397-138 US-09-925-297-738 US-09-925-490-4 US-09-925-43-2 US-09-864-761-47820 US-09-864-761-37443 US-09-893-737-262 US-09-893-737-262 US-09-965-529-25 US-09-934-483A-1 US-09-934-483A-5 US-09-934-483A-5 US-09-934-602-4 US-09-815-242-11790 US-09-815-242-11790 US-09-912-020-245 US-09-912-020-245 US-09-936-602-4 US-09-913-602-2 US-09-936-602-2
vodies	els 0; Gaps 0			Sequence 105, Appli Sequence 2, Appli Sequence 6860, Ap Sequence 4, Appli Sequence 2, Appli Sequence 4, Appli Sequence 47820, Ap Sequence 4602, Ap Sequence 18, Appl Sequence 25, Appli Sequence 5657, Appli Sequence 5, Appli Sequence 6, Appli Sequence 101, Appli Sequence 11790, Ap Sequence 27, Appli Sequence 291, App Sequence 21790, Ap Sequence 2184, App Sequence 184, App Sequence 5049, Ap Sequence 5049, Ap
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Result No.

Score

Query Match Length

DB

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Description

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

100.0 100.0 100.

96 179 478 478 487 504 713 713 713 713 713 713 859 27 100 114 114

Sequence 11, Appl sequence 247, App sequence 255, App sequence 4035, App sequence 183, App sequence 183, App sequence 183, App sequence 183, App sequence 184, App sequence 70, Appl sequence 179, App sequence 179, App sequence 179, App sequence 179, App sequence 315, App sequence 316, App sequence 316, App sequence 316, App sequence 376, App sequence 376, App sequence 376, App sequence 376, App sequence 315, App sequence 315, App sequence 315, App sequence 315, App

10 US-09-529-063-70 US-09-984-245-179 10 US-09-964-761-34868 12 US-10-001-870-116 12 US-09-950-933A-40 10 US-09-925-299-976 10 US-09-9815-242-10468

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RESULT 4
US-09-764-898-225
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LOCATION: (178)
OTHER INFORMATION: Xaa
US-09-764-853-847
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Sequence 225, Application US/09764898
Patent No. US20020090673A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, P.
FILE REFERENCE: PJZ01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 296
LENGTH: 179
TYPE: PRT
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 847
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SOFTWARE DEFECT: VI-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PJZ01
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NAME/KEY: SITE
LOCATION: (6)
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LOCATION: (164)
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FEATURE:
NAME/KEY: SITE
LOCATION: (6)
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LOCATION: (178)
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LOCATION: (164)
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Pred. No. 1.4e+02;
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SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 225
LENGTH: 478
TYPE: PRT
ORGANISM: Homo sapiens
US-09-764-898-225
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US-09-764-853-680
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Best Local S
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SEQ ID NO 680
LENGTH: 487
TYPE: PRT
ORGANISM: Homo sapiens
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PJZ06
CURRENT APPLICATION NUMBER: US/09/764,853
CURRENT FILING DATE: 2001-01-17
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
                                                             APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
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NAME/KEY: SITE
LOCATION: (6)
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YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
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                                                                                                                         PRIOR APPLICATION NUMBER: 60/062250
PRIOR EFILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR APPLICATION SUMBER: 60/064249
PRIOR APPLICATION NUMBER: 60/064311
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Best Local
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LENGTH: 504
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APPLICANT:
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APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C11
                                                                                                          PRIOR
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APPLICANT: Baker Kevin P
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APPLICATION NUMBER: 60/065311
FILING DATE: 1997-11-13
APPLICATION NUMBER:
                                           APPLICATION NUMBER: 60/077450 FILING DATE: 1998-03-10
                                                                           APPLICATION NUMBER: 60/066364 FILING DATE: 1997-11-21
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                            APPLICATION NUMBER: 60/077632
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Shelton, David L.
Stewart, Timothy A.
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Kljavin, Ivar J.
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Grimaldi, J. Christopher
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Shelton, David L.
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Williams, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Paoni,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Napier, Mary A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , Sherman
Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      James;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sophia S.
                                                                                                                                                                                                                                                                                                                                                                                                                                    , Daniel
P Mickey
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NUMBER: 60/078004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nicholas F
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f, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ivar J.
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Pred. No. 5.6e+02;
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DR APPLICATION NUMBER: 60/081070

DR FILING DATE: 1998-04-08

OR APPLICATION NUMBER: 60/081049

OR FILING DATE: 1998-04-08

IOR APPLICATION NUMBER: 60/081071

FILING DATE: 1998-04-08
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R APPLICATION NUMBER: 60/081838
R FILING DATE: 1998-04-15
R APPLICATION NUMBER: 60/082568
RF FILING DATE: 1998-04-21
R APPLICATION NUMBER: 60/082569
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R APPLICATION NUMBER: 60/080165
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APPLICATION 1998-03-30
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APPLICATION 1998-03-27
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APPLICATION NUMBER: 60/080333
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APPLICATION NUMBER: 60/080107
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APPLICATION NUMBER:
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FILING DATE: 1998-03-27
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PRIOR FILING DATE: 1998-04-22
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PRIOR APPLICATION NUMBER: 60/082796
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PRIOR FILING DATE: 1998-04-29
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PRIOR APPLICATION NUMBER: 60/083545
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Query Match Best Local Similarity

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CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
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DR FILING DATE: 1998-03-11
DR APPLICATION NUMBER: 60/077649
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FILING DATE: 1997-11-13
APPLICATION NUMBER: 60/066364
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                    FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/078910
FILING DATE: 1998-03-20
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Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William I.
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Grimaldi, J. Christopher
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Filvaroff,
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Kljavin, Ivar J.
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ff, Ellen
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PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
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PRIOR APPLICATION NUMBER: 60/081049
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PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
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OR APPLICATION NUMBER: 60/082700
OR FILING DATE: 1998-04-22
OR APPLICATION NUMBER: 60/082797
OR FILING DATE: 1998-04-22
OR APPLICATION NUMBER: 60/082796
OR FILING DATE: 1998-04-23
OR APPLICATION NUMBER: 60/083336
OR FILING DATE: 1998-04-27
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OR APPLICATION NUMBER: 60/082568
OR FILING DATE: 1998-04-21
OR APPLICATION NUMBER: 60/082569
OR FILING DATE: 1998-04-21
OR APPLICATION NUMBER: 60/082704
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APPLICATION NUMBER: 60/081952
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APPLICATION NUMBER: 60/081819
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APPLICATION NUMBER: 60/081203
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APPLICATION NUMBER:
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APPLICATION NUMBER: 60/080107
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APPLICATION NUMBER: 60/079920
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APPLICATION NUMBER: 60/079786
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APPLICATION NUMBER: 60/081817
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APPLICATION NUMBER: 60/081071
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Pred. No. 5.6e+02;
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APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides
TITLE OF INVENTION: Acids Encoding the Same
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FILING DATE: 1998-03-11
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           APPLICATION NUMBER: 60/079656 FILING DATE: 1998-03-26 APPLICATION NUMBER: 60/079664
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Baker Kevin P.
Botstein, David
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Shelton, David L.
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Grimaldi, J. C.
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OR APPLICATION NUMBER: 60/80328
OR FILING DATE: 1998-04-01
OR APPLICATION NUMBER: 60/08033
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FILING DATE: 1998-03-30
APPLICATION NUMBER: 60/080105
FILING DATE: 1998-03-31
FILING DATE: 1998-03-31

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RESULT 11
US-10-052-586-416
Sequence 416, Application US/10052586
Patent No. US20020127584A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
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OR APPLICATION NUMBER: 60/082569
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Goddard, Audrey
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Watanabe, Colin
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APPLICATION NUMBER: 60/082568 FILING DATE: 1998-04-21 APPLICATION NUMBER: 60/082569 FILING DATE: 1998-04-21 FILING DATE: 1998-04-1

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PR FILING DATE: 1998-04-29
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RFILING DATE: 1998-05-05
PR APPLICATION NUMBER: 60/084414
PR FILING DATE: 1998-05-06
PR APPLICATION NUMBER: 60/084639
RAPPLICATION NUMBER: 60/084639 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083559 APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER: 1998-04-29 60/083499 60/083496

APPLICATION NUMBER: 60/084640 FILING DATE: 1998-05-07 60/084643

APPLICATION NUMBER: FILING DATE: 1998-0: APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE: 1998-0 1998-05-15 1998-05-07 60/085573

R FILING DATE: 1998-05
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R APPLICATION NUMBER: 05 1998-05-15 1998-05-15 60/085579 60/085582 60/085580

FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085700
FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/086023
FILING DATE: 1998-05-18 APPLICATION NUMBER: FILING DATE: 1998-0 NUMBER: 60/086392 1998-05-22

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R APPLICATION NUMBER: 1998-05-28 1998-05-22 60/086486 60/087208 60/087098

FILING DATE: 1998-06-02 APPLICATION NUMBER: 60/087759 FILING DATE: 1998-06-02 APPLICATION NUMBER: 1998-05-28 60/087609 60/087827

R FILING DATE: 1998-06-02
R APPLICATION NUMBER: 60/0
R FILING DATE: 1998-06-03
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R FILING DATE: 1998-06-04 R APPLICATION NUMBER: (
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1998-06-05

60/088202 60/088167 APPLICATION NUMBER: 60/088033

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Matches
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          APPLICANT: FUKUSHIMA, DAIKICHI
APPLICANT: SHIBAYAMA, SHIRO
APPLICANT: TADA, HIDEAKI
TITLE OF INVENTION: POLYPEPTIDE, CDNA ENCODING
TITLE OF INVENTION: THE BOTH
FILE REFERENCE: Q58769
CURRENT APPLICATION NUMBER: US/09/529,063
CURRENT FILING DATE: 2000-04-07
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PRIOR APPLICATION NUMBER: PCT/JP98/04514
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; TYPE: PRT
; ORGANISM: Homo s
US-09-529-063-70
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PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: US 60/041,277
PRIOR FILING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: US 60/042,344
PRIOR FILING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: US 60/041,276
PRIOR APPLICATION NUMBER: US 60/041,276
PRIOR FILING DATE: 1997-03-21
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PRIOR APPLICATION NUMBER: JPP
PRIOR FILING DATE: 1997-10-07
NUMBER OF SEQ ID NOS: 117
SOFTMARE: Patentin Ver. 2.1
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PRIOR APPLICATION NUMBER: US 60/048,187
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,099
PRIOR FILING DATE: 1997-05-30
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PRIOR APPLICATION NUMBER: US 60/048,188
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,135
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CURRENT FILING DATE: 2001-10-29
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RAPPLICATION NUMBER: US 60/048,096
FILLING DATE: 1997-05-30
RAPPLICATION NUMBER: US 60/048,355
FILING DATE: 1997-05-30
RAPPLICATION NUMBER: US 60/048,160
FILING DATE: 1997-05-30
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Pred. No. 6.7e+02;
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; ORGANISM: Homo sapiens US-09-984-245-179
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PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
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PRIOR APPLICATION NUMBER: US 60/207,456
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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PRIOR APPLICATION NUMBER: US 60/054,804
PRIOR FILING DATE: 1997-08-05
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APPLICATION NUMBER: PCT/US01/00669
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APPLICATION NUMBER: US 60/234,687 FILING DATE: 2000-09-21
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Hanzel, David K.
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OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.8
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.8
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.7
OTHER INFORMATION: EXPRESSED IN LOUER SIGNAL = 10
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.8
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.5
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.2
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.2
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.9
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.3
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.5
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OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.6
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APPLICANT: Macina, Roberto
APPLICANT: Recipon, Herve
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
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LENGTH: 47
TYPE: PRT
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Best Local (
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                                                                                                                                                                                                                                                                                                                                 LENGTH: 62
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/252,189 PRIOR FILING DATE: 2000-11-21 NUMBER OF SEQ ID NOS: 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapien
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29 LLLVVA 34
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Pred. No.
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Search completed: January Job time: 5.77273 secs

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2003, 15:52:06

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Copyright

GenCore version 5.1.3 (c) 1993 - 2003 Compugen Ltd.

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Database
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Maximum DB seq
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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24	24	24	24	24	24	24	24	24	24	Score
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179	179	179	179	173	140	93	67	42	6	Query Match Length DB
22	22	22	22	23	23	23	21	21	23	DB
AAU17055	AAU18690	AAU18139	ABB10539	ABP39430	ABB90320	ABP05389	AAG61661	AAB34100	AAU11836	ID .
Human novel secret	Renal and cardiova	Novel human uterin	. Human cDNA SEQ ID	Staphylococcus epi	Human polypeptide	Human ORFX protein	Arabidopsis thalia	Human secreted pro	Peptide ligand for	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
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AAU14316	AAM24052	AAB42317	AAY02381	54	444	ABB05751	485	ABB90346	546	923	801	AAB44268	AAY41712	AAM93311	77	AAY15228	AAY71080	ABB81643	AAG90281	ABB81636	ABB10372	AAB59032	AAU16984	ABP28635	ABB52990	ABB91800	AAG82005	AAB42246	629	554	4262	081	4263	AAG10813
nove	Human EST encoded	$\overline{}$	ident	Human PRO14 protei	uman diag	Human G protein-co	PR0724 p	Human polypeptide	Human angiogenesis	PRO polypep	TANGO 1	Human PRO724 (UNQ3	Human PRO724 prote	polypep		receptor	<u></u>	Human zcytor19 pro	C glutamicum prote	Human zcytor19 pro	Human cDNA SEQ ID	t and ovaria	cre	s pol	Escherichia coli p	rbicidally ac	S. epidermidis ope	Human ORFX ORF2010	Novel human diagno	acteriu	is thali	is thali	is thali	Arabidopsis thalia

## ALIGNMENTS

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RESULT 1
AAU11836
Prion protein; Prp; ligand; octapeptide motif; scraple; prion-associated disease; Creutzfeldt-Jakob disease; Gerstmann-Straussler-Scheinker disease; fatal familial insomnia; feline spongiform encephalopathy; bovine spongiform encephalopathy; transmissible mink encephalopathy; exotic ungulate encephalopathy; chronic wasting disease.
         WPI; 2002-061944/08
                                 Hammond DJ,
                                                                                                       05-APR-2001; 2001WO-US11150
                                                                                                                                                                                                                                                                                                           26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                    AAU11836;
                                                                                                                                                                                                                                                                                                                                                         AAU11836 standard; peptide; 6 AA.
                                                         (VITE-) VI
                                                                                05-APR-2000; 2000US-0543188
                                                                                                                             18-OCT-2001.
                                                                                                                                                    WO200177687-A2
                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                   Peptide ligand for Prion protein, PrP, #11.
                                                         TECHNOLOGIES INC
                                 Wiltshire VR,
                                 Carbonell R,
                                 Shen
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Claim 11; Page 366; 419pp; English.

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a ligand of less than 6 kD that binds to a polypeptide containing the sequence GlyTyTGlyGlnPrOHisGlyGly (A) or an analogue that is the retro-inverso isomer of (A). The sequence A is an octapeptide motif from the prion protein (PrP). The ligands are identified by binding assays with the peptide (A) or peptides containing (A). The ligands are used for detecting prion proteins (or prions) in biological or environmental samples, e.g. for diagnosis, also for removing them from samples, for treating or retarding development of prion-associated diseases, especially Creutzfeldt-Jakob diseases (in latrogenic, new variant, familial or sporadic forms), but also Gerstmann-Straussler-Scheinker disease, fatal familial insommia,
   preservatives
                        New isolated nucleic acid molecules encoding 49 human secreted proteins used for preventing, treating or ameliorating medical conditions, for diagnosing pathological conditions or as food additives or
                                                                                                                                                                                                              19-MAR-1999;
10-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                         fungloide; ophthalmological; vulnerary; gene therapy; autoimmune disease; hyperproliferative disorder; neoplasm; cancer; cardiovascular disorder; cerebrovascular disorder; angiogenesis; nervous system disorder; lifection; ocular disorder; wound healing; skin aging; food additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          scrapie, bovine or feline spongiform encephalopathy, transmissible or exotic ungulate encephalopathy, or chronic wasting disease. The present sequence is a ligand of the invention.
                                                                                                                                                                                                                                                                                                                             WO200056755-A1
                                                                                                                                                                                                                                                                                                                                                                                              preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human secreted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB34100 standard;
                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                               16-MAR-2000; 2000WO-US06830.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New ligands for prion proteins, useful for detection or removal or
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DB; AAC59457.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            secreted protein; diagnosis; antiarthritic; immunosuppressive;
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                                                                                                                                              Ruben SM,
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                                                                                                                                                                                                            99US-0125361
99US-0169910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein sequence encoded by gene 9
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Pred. No. 7.8e+05;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mink
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AAG61661
ID AAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and vulnerary. The polynucleotides and polypeptides can be used to rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a nutoimmune diseases, hyperproliferative disorders e.g. neoplasms or cancer of the breast or liver, cardiovascular disorders, infections caused by bacteria, viruses and fungi and ocular disorders. The polypeptides can calso be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to cregenerate tissues and in chemotaxis. The polypeptides can also be as a food additive or preservative to increase or decrease storage capabilities. AAC59440 to AAC59448 and AAB34091 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                        09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
25-MAR-1999;
29-MAR-1999;
01-APR-1999;
06-APR-1999;
           08-APR-1999;
16-APR-1999;
                                                                                                                                           25-FEB-1999;
05-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and cells the genes are expressed in. Examples of activities include: antiarthritic; immunosuppressive; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; noctropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human secreted proteins given in human sequences and proteins AAB34216 represent human secreted polypeptide sequences and proteins homologous to them, which are given in the exemplification of the present homologous to them, which are given in the exemplification of the tissue invention. Human secreted proteins have activities based on the tissue invention.
                                                                                                                                                                                                                                                           EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                      Protein identification; signal transduction pathway; metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                         18-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                            25-FEB-2000;
                                                                                                                                                                                                                                                                                         Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                   hybridisation assay; genetic mapping; gene expression control;
                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana protein fragment SEQ ID NO: 80003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG61661 standard;
                                                                                                                                                                                                                                                                                                                           termination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LLLVIA 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 LLLVIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polynucleotide sequences given in AAC59449 to AAC59497 encode in secreted proteins given in AAB34092 to AAB34140. AAB34141 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       œ
                                                                                                                                                                                                                                                                                                                       sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                           2000EP-0301439
        990S-0125788.
990S-0126264.
990S-0126785.
990S-01267462.
990S-0128714.
990S-0129845.
                                                                                                                            99US-0123548
                                                                                                                                           99US-0123180
                                                                                                                                                           99US-0121825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 24; DB Pred. No. 1.3 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
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                                                                                                                                                                                                                                                                                                                                        promoter;
                                                                                                                                                                                                                                                                                                                                                       pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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TOUCH CONTROL OF THE	21-APR-1999 23-APR-1999 23-APR-1999 28-APR-1999 30-APR-1999 30-APR-1999 06-MAY-1999 06-MAY-1999 06-MAY-1999 07-MAY-1999
990S-0134218 990S-0134219 990S-0134219 990S-0134219 990S-0134219 990S-01342629 990S-0135353 990S-01356782 990S-0136782 990S-0136782 990S-0137528 990S-0139454 990S-0139453 990S-0140695 990S-0140695 990S-0142897 990S-0142897 990S-0142897 990S-0142897 990S-0142897 990S-0144085 990S-01443333 990S-01443333	99US-0130449. 99US-0130510. 99US-0130891. 99US-0132449. 99US-0132407. 99US-0132484. 99US-0132486. 99US-0132487. 99US-0132863.
מר על היה על היה על היה ע	ס ס ס ס ס ס ס ס ס ס ס ס ס ס ס ס ס ס ס
23 - JUL - 1999 26 - JUL - 1999 27 - JUL - 1999 27 - JUL - 1999 28 - JUL - 1999 29 - JUL - 1999 20 - AUG - 1999 00 - AUG - 1999 00 - AUG - 1999 00 - AUG - 1999 10 - AUG - 1999 11 - AUG - 1999 11 - AUG - 1999 12 - AUG - 1999 13 - AUG - 1999 14 - AUG - 1999 15 - AUG - 1999 16 - AUG - 1999 17 - AUG - 1999 18 - AUG - 1999 19 - AUG - 1999 10 - AUG - 1999 11 - AUG - 1999 11 - AUG - 1999 12 - AUG - 1999 13 - AUG - 1999 14 - SEP - 1999 27 - AUG - 1999 28 - SEP - 1999 29 - SEP - 1999 20 - SEP - 1999 21 - SEP - 1999 21 - SEP - 1999 22 - SEP - 1999 23 - SEP - 1999 24 - SEP - 1999 26 - OCT - 1999 17 - OCT - 1999 18 - OCT - 1999 18 - OCT - 1999 19 - OCT - 1999 11 - OCT - 1999	20 -JUL-1999; 20 -JUL-1999; 20 -JUL-1999; 21 -JUL-1999; 21 -JUL-1999; 22 -JUL-1999; 22 -JUL-1999; 22 -JUL-1999; 22 -JUL-1999; 23 -JUL-1999; 23 -JUL-1999;
990S-0145214 990S-0145276 990S-0145214 990S-0145911 990S-0145388 990S-0147388 990S-0147303 990S-0147303 990S-0147303 990S-0147416 990S-0147416 990S-0147416 990S-0147416 990S-0148341 990S-0149722 990S-0149722 990S-0149723 990S-0149723 990S-0151086	9US-014435 9US-014463 9US-014481 9US-014508 9US-014508 9US-014508 9US-014508 9US-014508 9US-014508

14-OCT-1999; 14-OCT-1999; 14-OCT-1999;

8-OCT-1999; 1-OCT-1999;

99US-0160741 99US-0159637 99US-0159638 99US-0159331

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RESULT 4
ABP05389
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Best Local :
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22-OCT-1999;
22-OCT-1999;
25-OCT-1999;
25-OCT-1999;
 Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders .
                                                                                                                       30-MAY-2000;
29-AUG-2000;
                                                                                                                                                                          06-DEC-2001
                                                                                                                                                                                               WO200192523-A2
                                                                                                                                                                                                                                      myasthenia gravis
                                                                                                                                                                                                                                                 autoimmune
                                                                                                                                                                                                                                                                           hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
                                                                                                                                                     29-MAY-2001; 2001WO-US10836
                                                                                                                                                                                                                   Homo
                                                                                                                                                                                                                                                                                                           Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
                                                                                                                                                                                                                                                                                                                                 Human ORFX protein sequence SEQ ID NO:10760.
                                                                                                                                                                                                                                                                                                                                                       25-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                           ABP05389;
                                                                                                 (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                   hypertension; hypothyroidism; cholesterol ester storage disease;
                                                                                                                                                                                                                                                                                                                                                                                               ABP05389 standard;
                                                                                                                                                                                                                                                          lmmune deficiency;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1-OCT-1999;
1-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 LLLVIA 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -OCT-1999;
                                                          2002-106308/14.
                                                                                                                                                                                                                  sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLLVIA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conserv
                                                ABN21141.
                                                                              RA,
                                                                                                                                                                                                                                                disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                       2000US-206132P
2000US-228716P
                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                              Leach MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0161404
99US-0161406
99US-0161359
99US-0161360
99US-0161360
99US-0161920
99US-0161920
99US-0161920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0160814.
99US-0160815.
99US-0160980.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0160981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0160768
99US-0160770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0162142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0160767
                                                                                                                                                                                                                                                         immune disorder; infectious disease,
                                                                                                                                                                                                                                                                                                                                                                                               Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                               rheumatoid arthritis; autoimmune thyroiditis,
                                                                                                                                                                                                                                                                                                                                                                                               93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 24; DB 21;
Pred. No. 2.2e+02;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
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diseases, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also
                                                                                                                                                   bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reportusion injury in various tissues and conditions resulting from
                                                                                                                                                                                                                                                                                                                                     transplantation, cardiovascular diseases, diabetes mellitus, systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table in the specification). ABMI5762 to ABM27525 encode the human ORFX proteins given in ABP00010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating syndrome associated with ORFX-associated disorder. ORFX polynucleotide
Sequence
                                                                           N.B. The sequence data for this patent did not form specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                         sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders, disorders related to organ
                                                  at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                             systemic cytokine damage.
                                                                                                                                                                                                                                    useful for treating burns, incisions,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID 10760; 1037pp; English.
93
ĄΑ;
                                                                                                                                                                                                                                       ulcers,
                                                                                                                                                                                                                                    for treating osteoporosis,
                                                                           part of the printed directly from WIPO
                                                                                                                                                                                                                                                                                                                                              infectious
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Query Match Best Local S Matches 6 19 LLLVIA Local Similarity nes 6; Conserv 1 LLLVIA 6 24 Conservative 100.0%; 0 Score 24; DE Pred. No. 3.2 0; Mismatches DB 23; 3.2e+02; 0 Length Indels 0;

Gaps

0

## RESULT 5 ABB90320

Ър Q

ABB90320 standard; Protein; 140 AA.

24-MAY-2002 (first entry)

Human polypeptide SEQ ID NO 2696.

Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabettc; antiinflammatory; antiucer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasituc; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder cardiant; gene therapy; cancer; immune disorder; cardiov; neurological disease; infection; human; secreted protein

Homo sapiens

WO200190304-A2

18-MAY-2001; 2001WO-US16450

19-MAY-2000; 2000US-205515P

(HUMA-) HUMAN GENOME SCI INC

Birse CE, Rosen CA;

WPI; 2002-122018/16 N-PSDB; ABL90729.

0;

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ABP39430
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Best Local Similarity
"-+-hes 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epileps; and (f) infectious diseases such as viral, bacterial, fungand parasitic infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB89040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification.
              Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format dir from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                       Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections
                                                                                       WPI; 2002-381255/41.
N-PSDB; ABN91975.
                                                                                                                                                                                              14-AUG-1997;
08-NOV-1997;
                                                                                                                                                                                                                                                                                                       US6380370-B1
                                                                                                                                                                                                                                                                                                                                  Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus
                                                                                                                                  Doucette-Stamm LA,
                                                                                                                                                                                                                                          13-AUG-1998;
                                                                                                                                                                                                                                                                         30-APR-2002
                                                                                                                                                                                                                                                                                                                                                                antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                            24-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP39430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABP39430 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gastrointestinal, pulmonary, cardiovascular, renal and proliferative
disorders -
                                                                                                                                                                (GENO-) GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prevention of neural,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LLLVIA 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLLVIA 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140
              SEQ ID 4275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                                                                THERAPEUTICS CORP
                                                                                                                                                                                              97US-055779P.
97US-064964P.
                                                                                                                                                                                                                                                                                                                                  epidermidis
                                                                                                                                                                                                                                                                                                                                                              gene therapy
                                                                                                                                                                                                                                                                                                                                                                              epidermidis; open reading frame; ORF; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                            epidermidis ORF amino acid sequence SEQ ID NO:4275
                                                                                                                                                                                                                                          98US-0134001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein; 173
                                                                                                                                  Bush
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .0%;
         267pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 24;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 23;
5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bacterial, fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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RESULT 7
ABB10539
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Best Local 9
                                                                                                                                                                                                                                                         31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
                                                                       11-JUL-2000;
11-JUL-2000;
14-JUL-2000;
26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
                                                                                                                                                                                                                       18-APR-2000;
19-MAY-2000;
07-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                       07-JUL-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         muscular disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; renal disorder;
                                                                                                                                                                                               28-JUN-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB10539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB10539 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                               17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                       02-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USPTO web site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 LLLVIA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 LLLVIA 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene therapy; neural disorder; immune system disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO: 847.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
2000US-180628P
2000US-18464P
2000US-188350P
2000US-189874P
2000US-199129P
2000US-205515P
2000US-205515P
2000US-216487P
2000US-216487P
2000US-216880P
2000US-217487P
2000US-22513P
2000US-225266P
2000US-225266P
2000US-225266P
2000US-225266P
2000US-225270P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                               2001WO-US01349
                                                                                                                                                                                                                                                                                                                                                                                                                                                disorder; inflammation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 173;
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RESULT 8
AAU18139
ID AAU1
XX
AC AAU1
XX
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Matches 6
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08-NOV-2000
08-NOV-2000
08-NOV-2000
17-NOV-2000
17-NOV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides human cDNAs, proteins and related gen DNAs. These can be used in the treatment of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders and inflammation. The present sequences are suppressed to the present sequences and proliferative disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated nucleic acid \mathfrak n polypeptide is used in condition -
                        AAU18139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-476161/51.
N-PSDB; ABA06761.
                                                                           AAU18139 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                      1 LLLVIA 6
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134 LLLVIA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein of the
                                                                                                                                                                                                                                                                                                               Similarity 100 6; Conservative
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2000US - 246611P

2000US - 246613P

2000US - 24920P

2000US - 249210P

2000US - 249211P

2000US - 249211P

2000US - 249213P

2000US - 249218P

2000US - 249264P

2000US - 249264P

2000US - 249264P

2000US - 249269P

2000US - 249269P

2000US - 2511869P

2000US - 2511869P

2000US - 25198P

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                                                                                                                                                                                                                                                                                                                                                                                                                       ΑA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SC,
                                                                           Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             847; 859pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    molecule encoding an inflammation-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preventing, treating or ameliorating a
                                                                                                                                                                                                                                                                                                                                        .0%;
                                                                           179
                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                             Score 24; DE
Pred. No. 6.6
); Mismatches
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                                                                           A
                                                                                                                                                                                                                                                                                                       DB 22;
. 6.6e+02;
-~ 0;
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                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genomic
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14-AUG-2000 11-AUG-2000 11-AUG-2000 12-AUG-2000 22-AUG-2000 23-AUG-2000 23-AUG-2000 23-AUG-2000 23-AUG-2000 20-OCT-2000 20-SEP-2000 20-SEP-2000 20-SEP-2000 20-SEP-2000 20-SEP-2000 20-SEP-2000 20-SEP-2000 20-SEP-2000 20-SEP-2000 21-SEP-2000 21-SE

2000US-22575PP
2000US-22575PP
2000US-22668BP
2000US-22668BP
2000US-22688BP
2000US-227009P
2000US-229343P
2000US-229343P
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2000US-229343P
2000US-231243P
2000US-24677P
2000US

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Novel human uterine labour; menstru (200155201-A1 (2001552001-A1 (2001552001-A1 (2001552001-A1 (2001552001-A1 (2001552001-A1 (2001552001-A1 (2001552001-A1 (2001552001-A1 (20015520001-A1 (2
first entifity tentifity motility motil
lity-association polypeptide association disorder; uterus gene therapy.  317.  317.  317.  317.  317.  317.  318.  326.  327.  346.7.  447.  447.  448.  3214.  447.  448.  3214.  448.  3214.  448.  3214.  448.  334.  344.
ls; Fregnancy;
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14 - SEP - 2000; 21 - SEP - 2000; 25 - SEP - 2000; 25 - SEP - 2000; 27 - SEP - 2000; 29 - SEP - 2000; 29 - SEP - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 21 - OCT - 2000; 22 - OCT - 2000; 23 - OCT - 2000; 24 - OCT - 2000; 25 - OCT - 2000; 26 - OCT - 2000; 27 - OCT - 2000; 28 - NOV - 2000; 29 - OCT - 2000; 20 - OCT - 2000; 21 - OCT - 2000; 20 - OCT - 2000; 21 - OCT - 2000; 21 - OCT - 2000; 22 - OCT - 2000; 23 - OCT - 2000; 24 - OCT - 2000; 25 - OCT - 2000; 26 - OCT - 2000; 27 - OCT - 2000; 28 - NOV - 2000; 29 - OCT - 2000; 20 - OCT - 2000; 21 - OCT - 2000; 22 - OCT - 2000; 23 - OCT - 2000; 24 - OCT - 2000; 25 - OCT - 2000; 26 - OCT - 2000; 27 - OCT - 2000; 28 - OCT - 2000; 29 - OCT - 2000; 20 - OCT - 2000; 21 - OCT - 2000; 21 - OCT - 2000; 22 - OCT - 2000; 23 - OCT - 2000; 24 - OCT - 2000; 25 - OCT - 2000; 26 - OCT - 2000; 27 - OCT - 2000; 28 - OCT - 2000; 29 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 21 - OCT - 2000; 22 - OCT - 2000; 23 - OCT - 2000; 24 - OCT - 2000; 25 - OCT - 2000; 26 - OCT - 2000; 27 - OCT - 2000; 28 - OCT - 2000; 29 - OCT - 2000; 20 - OCT - 2000; 21 - OCT - 2000; 22 - OCT - 2000; 23 - OCT - 2000; 24 - OCT - 2000; 25 - OCT - 2000; 26 - OCT - 2000; 27 - OCT - 2000; 20 - O
2000US -0233064 2000US -0233065 2000US -023423 2000US -0234998 2000US -0234998 2000US -0235836 2000US -0235836 2000US -0236369 2000US -0236610 2000US -0236610 2000US -0236610 2000US -0236611 2000US -0236921 2000US

2000US-0184664. 2000US-0186350. 2000US-0189874. 2000US-0190076. 2000US-0198123.

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Best Local S
Matches 6
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08-DEC-2000;
08-DEC-2000;
11-DEC-2000;
05-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to the isolation of novel human uterine motility-association polypeptides, and cDNA (AAS28936-AAS28994) and genomic sequences encoding for these polypeptides. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of diseases associated with uterine motility such as pregnancy and labour, and menstrual disorders. The polynucleotide sequences of the invention are also useful in gene therapy. AAU18094-AAU818152 represent novel human uterine motility-associated prognosis of disorders. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
           31-JAN-2000; 2000US-0179065.
04-FEB-2000; 2000US-0180628.
                                                                                                                                                                                 Human; antiinflammatory; neuroprotective; immunomodulator; vulnerary; cardiovascular; cytostatic; nephrotropic; antianaemic; nephritis; immunosuppressive; kidney disorder; renal failure; hypertension; cardiovascular disorder; myocardial infarction; blood disorder; anaem blood coagulation disorder; electrolyte imbalance disorder; cancer; hyponatraemia; hyperkalaemia; nephastic disorder; nephtoma;
                                                17-JAN-2001; 2001WO-US01359
                                                                                                                                                                                                                                                                                                                          AAU18690;
                                                                                                                                                                                                                                                                                                                                                 AAU18690 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated polypeptide and nucleic acid molecules for treating, preventing and/or prognosing disorders related to uterine motility e.g. disorders associated with pregnancy and the menstrual cycle -
                                                                                                 WO200155328-A2
                                                                                                                          Ното
                                                                                                                                              autoimmune disease; inflammatory disease; reproductive system disorder; endocrine disorder; neural activity; neurological disorder; wound healing; respiratory disorder.
                                                                                                                                                                                                                                                                         Renal and
                                                                                                                                                                                                                                                                                                  21-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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les 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LLLVIA 6
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                                                                                                                        sapiens
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                                                                                                                                                                                                                                                                       cardiovascular-associated protein,
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2000US-0251989.
2000US-0251990.
2000US-0254097.
2000US-0259678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ID No 115;
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                                                                                                                                                                                                                                                                                                                                                 Protein; 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
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Pred. No. 6.6e+02;
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                                                                                                                                                                                                                                                                       Seq ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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                                                                                                                                                                                                            anaemia;
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              14 - SEP - 2000

14 - SEP - 2000

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14 - SEP - 2000

21 - SEP - 2000

21 - SEP - 2000

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29 - SEP - 2000
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11-JUL-2000;
11-JUL-2000;
14-JUL-2000;
26-JUL-2000;
26-JUL-2000;
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18-AUG-2000

22-AUG-2000

22-AUG-2000

23-AUG-2000

30-AUG-2000

01-SEP-2000

01-SEP-2000

01-SEP-2000

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05-SEP-2000

06-SEP-2000

06-SEP-2000

08-SEP-2000

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19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
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02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
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2000US-0233064. 2000US-0233065. 2000US-0234223. 2000US-0234297. 2000US-0234998. 2000US-02349484.

2000US-0235834. 2000US-0235836. 2000US-0236327. 2000US-0236367. 2000US-0236368. 2000US-0236369. 2000US-0236370. 2000US-0236370. 2000US-0236370. 2000US-0232080. 2000US-0232081. 2000US-0231968. 2000US-0232397. 2000US-0232398.

2000US-0232399. 2000US-0232400. 2000US-0232401. 2000US-0233063. 2000US-0230438. 2000US-0231242. 2000US-0231243. 2000US-0231244. 2000US-0231244. 2000US-0231413.

2000US-0229509 2000US-0229513 2000US-0230437

2000US-0227182. 2000US-0227009. 2000US-0228924. 2000US-0229924. 2000US-0229287. 2000US-0229343. 2000US-0229344. 2000US-0229345.

2000US-0225759 2000US-0226279 2000US-0226681 2000US-0226868 2000US-0220964. 2000US-0224518. 2000US-0224519. 2000US-0225213.

2000US-0219467 2000US-0214886 2000US-0215647 2000US-0215647 2000US-0217487 2000US-0217487 2000US-0217487 2000US-0218290 2000US-0218290

2000US-0225267. 2000US-0225268. 2000US-0225270.

2000US-0225214 2000US-0225266

2000US-0225447 2000US-0225757

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05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
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20-OCT-2000

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20-OCT-2000

20-OCT-2000

01-NOV-2000

08-NOV-2000

                                                                                                                                                                                                                                         01-DEC
05-DEC
       New polynucleotides and polypeptides, useful for diagnosing, treating, preventing or prognosing e.g. kidney, cardiovascular, blood, electrolyte imbalance or neoplastic disorders, autoimmune diseases,
                                                                                         Rosen
                                                       N-PSDB;
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                                                                                                              (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                    17-NOV-2000;
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                                                      2001-488787/53.
DB; AAS30211.
                                                                                         CA,
                                                                                       Barash SC,
                                                                                                                                                                                2000US-0249244

2000US-0249245

2000US-0249265

2000US-0249297

2000US-0249299

2000US-0249299

2000US-025036

2000US-0250391

2000US-0251988

2000US-02551479

2000US-0251868

2000US-0251868
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2000US-0246527
2000US-0246528
2000US-0246609
2000US-0246610
2000US-0246611
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2000US-0249207
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2000US-0249209
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2000US-0241787.
2000US-0241808.
2000US-0241809.
2000US-0241826.
2000US-0244617.
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2000US-0246476.
2000US-0246477.
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2000US-0237040.
2000US-0239935.
2000US-0239937.
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2000US-0251990
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2000US-0249213
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2000US-0246523
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2001US-0259678
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2000US-0249218
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2000US-0249215
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                                                                                                               SCI INC.
                                                                                         Ruben
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RESULT 10
AAU17055
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Best Local S
Matches 6
31-JAN-2000
04-FEB 2000
24-FEB 2000
02-MAR-2000
16-MAR-2000
17-MAR-2000
19-MAY-2000
07-JUN-2000
28-JUN-2000
07-JUL-2000
07-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to novel nucleic acids and polypeptides useful fidiagnosing, treating, preventing and/or prognosing disorders related to these polypeptides. The polynucleotides are especially useful in the diagnosis, prognosis, prevention and/or treatment of diseases which include kidney disorders (e.g. renal failure or nephritis), cardiovascular disorders (e.g. hypertension or myocardial infarction), blood disorders (e.g. anaemia or blood coagulation disorders),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            electrolyte imbalance disorders (e.g. hyponatraemia or hyperkalaemia), neoplastic disorders (e.g. nephtoma or renal cell cancer), autoimmune diseases, cancers, inflammatory diseases, reproductive system disorders, endocrine disorders, neural activity and neurological disorders, wound healing and respiratory disorders. AAU18644-AAU18715 represent the novel human renal and cardiovascular associated amino represent the novel human renal and cardiovascular associated amino
                                                                                                                                                                                                                                                                                                                                                                                       Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; no neuroprotective; antibacterial; vicucide; fungicide; op vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cerebrovascular disorder; cerebral ischaemia; angiogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   did not form part of the printed specification, but was obtained electronic format directly from WIPO at:
                                                                                                                                                                                                                                                                                                                                                          cerebrovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocular corneal infection; wound healing; epithelial cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU17055 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1;
                                                                                                                                                                                                                     17-JAN-2001;
                                                                                                                                                                                                                                                    02-AUG-2001
                                                                                                                                                                                                                                                                                 WO200155441-A2
                                                                                                                                                                                                                                                                                                                                               skin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human novel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acid sequences of the invention. Note: The sequence data for this patent
                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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2000US-0189874.
2000US-019076.
2000US-0198123.
2000US-0205515.
2000US-0209467.
2000US-0214886.
2000US-0215135.
2000US-021647.
2000US-0216647.
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                                                                                                                                      2000US-0180628.
2000US-0184664.
2000US-0186350.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                     2001WO-US01320
                                                                                                                                                                                                                                                                                                                                             food
                                                                                                                                                                                     2000us-0179065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
                                                                                                                                                                                                                                                                                                                                            additive; preservative; antiproliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein; 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .0%; Score 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID 296.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      nootropic;
opthalmalogical;
                                                                                                                                                                                                                                                                                                                                                                                                         cardiac arrest;
                                                                                                                                                                                                                                                                                                                                                                            ocular disorder;
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The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or constitution.
                                                                                                                                                                                                                                                                                                                                                                                                                              20-0CT-2000
01-NOV-2000
08-NOV-2000
017-NOV-2000
17-NOV-2000
17-NO
                                                                                                                                                                                                      Novel polypeptides and polynucleotides useful as diagnostic reagents diagnose diseases or disorders associated with aberrant expression or activity of polypeptides, for treating blood clotting disorder, haemophilia
                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                   WPI; 2001-476222/51
N-PSDB; AAS26960.
                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN
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26-JUL-2000 14-AUG-2000 12-AUG-2000 13-AUG-2000 13-AUG-2000 14-AUG-2000 15-SEP-2000 16-SEP-2000 17-SEP-2000 18-SEP-2000 19-SEP-2000 10-SEP-2000 10-SEP-2000 11-SEP-2000 11-SE

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2000US-0217487
2000US-0225263
2000US-0235263
2000US-0235293
2000US-0241786

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RESULT 11
AAG10813
                                                                                                                                                                                                                                                                                                                                                       cc immunosorbant assays (ELISA). Disorders which are diagnosed or treated cc include autoimmune diseases e.g. rheumatoid arthritis, cc hyperproliferative disorders e.g. neoplasms of the breast or liver, cc cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, revous system disorders e.g. cardiac arrest by bacteria, viruses and fungi can ocular disorders e.g. corneal infection, and many other can also compared to aid wound healing and epithelial cell proliferation, to be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, confactors and other nutritional components. The present
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Best Local S
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 25-FEB-1999

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              termination sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana protein fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG10813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG10813 standard; Protein;
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llarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mapping; gene
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Pred. No. 6.6e+02;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO: 9285.
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    14 - MAY 1999
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99US-0139763

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99US-014254

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99US-014354

99US-014408

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RESULT 12

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28 OCT 1999;
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Similarity 100
6; Conservative
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99US-0161361.
99US-0161361.
99US-0161920.
99US-0161923.
99US-0161993.
99US-0162142.
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Pred. No. 6.7e+02;
Mismatches 0;
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promoter;
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Note: The sequence data for this patent did not form part of the printed as pecification, but was obtained in electronic format directly from WIPO at the property of the printed at the property of the
                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; SEQ ID No 6740; 1069pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
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N-PSDB; AAS59526.
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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3: pir3:*
4: pir4:*
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Match Length DB
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## ALIGNMENTS

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15K cysteine-rich outer membrane protein - Chlamydia trachomatis (serotype C)
C;Species: Chlamydia trachomatis
C;Species: Chlamydia trachomatis
C;Date: 12-Jan-1993 #sequence_revision 12-Jan-1993 #text_change 10-Dec-1999
C;Accession: F43584; S24274
R;de la Maza, L.M.; Fielder, T.J.; Carlson, E.J.; Markoff, B.A.; Peterson, E.M.
Infect. Immun. 59, 1196-1201, 1991
A;Title: Sequence diversity of the 60-kilodalton protein and of a putative 15-kilodal
A;Reference number: A43584; MUID:91147205; PMID:1997423
A;Accession: F43584
                                                                                                                               A; Molecule type: DNA
A; Residues: 1-152 <DEL>
A; Cross-references: EMBL:X54388; NID:g40760; PIDN:CAA38258.1; PID:g40762
C; Superfamily: Chlamydia 15K cysteine-rich outer membrane protein
C; Keywords: membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 282, 754-759, 1998

A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia A;Reference number: A71570; MUID:99000809; PMID:9784136
A;Accession: C71515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable 15kda cysteine-rich protein - Chlamydia trachomatis (serotype D, strain UW3/C;Species: Chlamydia trachomatis
C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 10-Dec-1999
C;Accession: C71515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-150 < ARN>
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                                          Best Local Similarity
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                                            0;
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Pred. No.
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Cross-reterences. University of the state of
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A: Map position: 2
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C;Genetics:
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A; Residues: 1-183 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jothetical protein At2g22170 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: G84609
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                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana A; Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     euss, D.; Nierman, W.C.; Nature 402, 761-768, 1999
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R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequer
Nature 406, 151-157, 2000
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Best Local
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Residues: 1-159 <SIM>
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53 LLLVIA 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
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probable integral membrane protein - Streptomyces coelicolor (;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 03:Dec-1999 #sequence_revision 03:Dec-1999 #text_char C;Accession: T36065
R;Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Be submitted to the EMBL Data Library, November 1998
A;Reference number: Z21595
A;Accession: T36065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 17454 A; Cross-references: DDBJ: AP000061;
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C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: C72609
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A;Introns: 42/1; 93/3; 141/3; 188/2
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A;Residues: 1-224 <DAV>
A;Reservers: EMBL.AF022977; PIDN:AAB88611.1; GSPDB:GN00023; CESP:ZK994.4
A;Experimental source: strain Bristol N2; clone ZK994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Davidson, S.; Wohldmann, P. submitted to the EMBL Data Library, September 1997 submitted to the EMBL Data Library, September 1997 A;Description: The sequence of C. elegans cosmid ZK994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein ZK994.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-232 <KAW>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, A; Reference number: A72450; MUID:99310339; PMID:10382966
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DNA Res. 6, 83-101, 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary
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||||||
82 LLLVIA 87
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Pred. No.
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No.
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hypothetical protein C54H2.5 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #tC;Accession: T29611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Variety: PCC 6803
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change C;Accession: S17746; S74588; S14861
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Cross-references: EMBL:X58128; NID:g47506; PIDN:CAA41130.1; PID:g47508
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.
R;Kanekokumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuc
DNA Res. 3, 109-136, 1996
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A; Residues: 1-276 <L:
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Plant Mol. Biol. 17, 641-652, 1991
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A; Cross-references: EMB
submitted to the EMBL Data Library, May 1996
                   R; Fulton,
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A; Residues: 1-276 < KAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: nucleic acid sequence not shown;
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Matches
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7-44/Domain: transmembrane #status predicted <TM1>
63-82/Domain: transmembrane #status predicted <TM2>
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lternate names: ATP synthase chain a
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Pred. No. 3.5
); Mismatches
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                                                      15-Oct-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translation not shown
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3.1e+02;
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A; Molecule type: DNA
A; Residues: 1-284 <BLA>
A; Residues: 1-284 <BLA>
A; Cross-references: EMBL:X56466; NID:g45509; PIDN:CAA39839.1;
C; Superfamily: signal peptidase I
C; Keywords: hydrolase; serine proteinase; transmembrane prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein slr0241 - C; Species: Synechocystis sp. A; Variety: PCC 6803
                                                                                                                                                                             A; Reference number: A; Accession: S22414
                                                                                                                                                                                                  C;Species: Pseudomonas fluorescens C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text C;Accession: S22414
R;Black, M.T.; Munn, J.G.R.; Allsop, A.E.
Blochem. J. 282, 539-543, 1992
A;Title: On the catalytic mechanism of prokaryotic leade A;Reference number: S22413; MUID:92189595; PMID:1546969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:D90900; GB:AB001339; NID:g1651768; PIDN:BAA16703.1; PID:d101 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
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A; Residues: 1-281 <KAN>
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A;Accession: S74551
A;Status: preliminary
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A; Introns: 23/3:
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A; Residues: 1-277 < FUL>
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A;Reference number: 220651
A;Accession: T29611
A;Status: preliminary; translated
                                                                                                                                                            A; Status: preliminary
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les 6; Conserv
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                                                                                                                                                                                                                                                                                                                                             names: leader peptidase
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nilarity 100.
Conservative
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                                                           serine proteinase; transmembrane protein
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100.0%;
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Pred. No. 3.5
); Mismatches
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Score 24;
Pred. No.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas fluorescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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DB 2;
3.6e+02;
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                Length 284;
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                                                                                                                                                                                                                       peptidase
                                                                                                     PID:g45511
                                                                                                                                                                                                                                                                                                         19-May-2000
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RESULT 14
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C;Superfamily: signal peptidase I
C;Keywords: hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: H83550
R;Stover, C.K.; Pham, X.Q.;
adman, S.; Yuan, Y.; Brody,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
C;Species: Agrobacterium tumefaciens
                                                                                                                                                                                                                                                   C; Superfamily: oligopeptide permease protein oppB
                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-295 <KUR>
A;Cross-references: GB:AE007870; PIDN:AAK89937.1; PID:g15159892; GSPDB:GN00170
                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: G98301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical ABC transporter permease protein yddQ AGR_L_2741 [imported] - Agrobacterium C;Species: Agrobacterium tumefaciens C;Date: 22-Oct_2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable signal peptidase I (EC 3.4.21.89) PA0768 [similarity] - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 24-May-2001
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                              ABC transporter,
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A; Reference number: A82950;
ccession: H83550
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                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
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                                                                                                                                                                                                                                                                                                         Genetics:
                                                                                                                                                                                                                      Query Match
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Best Local
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nes 6; Conserv
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                              membrane spanning
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                                                                                                                                                                                  100.0%; Score 24; DB 2; 1
100.0%; Pred. No. 3.7e+02;
0. Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                               the Plant Pathogen and Biotechnology Agent Agrobacterium tun PMID:11743194
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L.L.; Coulter, S.N.; Folger, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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                              protein
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Pred. No. 3.6e+02;
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                              Atu3458 [imported]
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K.R.; Kas,
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                            Agrobacterium
                                                                                                                                                                                      0;
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Larbig,
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Markelz, B.
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Job time : 10.9545
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January

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2003, 15:33:17

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C;Accession: AD0306
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G. il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel Nature 413, 523-527, 2001
Nature 413, 523-527, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McCl; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam ster, E.W.
                                                                                                                                                                                                     A; Gene: YPO2507
                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-295 <K
                                                                                                                                                                                                                                                                                                                                                     A; Reference number: AB0001; A; Accession: AD0306
                                                                                                                                                                                                                                                                                                                                                                            A; Title: Genome sequence of Yersinia pestis, the causative agent of plague. A; Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: AD0306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable membrane protein YPO2507 [imported] - Yersinia pestis (strain CO92)
C; Species: Yersinia pestis
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Best Local Similarity
% 6; Conserva
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A;Cross-references: GB:AE008689; PIDN:AAL44271.1; PID:g17741857; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: AF
A; Accession: AI2981
A; Status: preliminary
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                                                                                                                                                                                                                                                    A; Cross-references: GB: AL590842;
                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
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                                                                                                  Best Local Similarity
Matches 6; Conser
                                                                                                                                               Query Match
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Pred. No. 3.7e+02;
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Pred. No. 3.7e+02;
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Maximum DB :
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Maximum Match 100%
Listing first 45 summaries
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15 kDa cysteine-rich outer membrane protein
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia NCBI_TaxID=813;
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Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R.,
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Science 282:754-759(1998).
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Mesyanzhinov V., Ruger W., Stidham T., Thomas E.;
"Bacteriophage T4 genome analysis.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
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Viruses; dsDNA viruses,
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                                                                                                                 (RBS) INTO ELEMENTARY BODIES (EBS). INTEGRITY OF THE EBS OUTER ENVELOPE. SUBCELLULAR LOGATION: Outer membrane.
                              SWISS-PROT entry is copyright. It is produced through a collabeen the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-kilodalton protein between the trachoma and venereum blovars of Chlamydia trachomatis."; Infect. Immun. 59:1196-1201(1991).
-i- FUNCTION: ASSOCIATED WITH DIFFERENTIATION CELEMENTARY BODIES (EBS). IT IS N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRPC_CHLTR STANDARD; PRT; p26756; 01-AUG-1992 (Rel. 23, Created) 01-AUG-1992 (Rel. 23, Last sequence 15-JUN-2002 (Rel. 41, Last annotatio 15 kDa cysteine-rich outer membrane
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Outer membrane; Complete proteome.
SEQUENCE 150 AA; 15985 MW; 77A6FB7CC8FADB34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chlamydia trachomatis. Bacteria; Chlamydiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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al 18.6 kDa protein i
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a protein in P143-LEF5 intergenic region.
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Cryptophlebia Hypothetical

leucotreta granulosis

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RESULT 6
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DE ATP SY
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                                                                                                                                         Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sujurra M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruc K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S.; Yamada M., Yasuda M., Tabata S.; "Squence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome organization of the DNA-binding protein gene region of Cryptophlebia leucotreta granulosis virus is closely related to of nuclear polyhedrosis viruses.";

J. Gen. Virol. 75:1815-1820(1994).

-!- SIMILARITY: TO CORRESPONDING ORF IN ACMNPV AND OPMNPV.

-!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 IS THE INITIATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical SEQUENCE 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                            PCC
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                                                                                                                                                                                                                                                                                                MEDLINE=97061201; PubMed=8905231;
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                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                         Plant
                                                                                                                                                                                                                                                                                                                                                                                           "The atpl and atp2 operons of the cyanobacterium Synechocystis sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94292936; PubMed=8021613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=35254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; dsDNA
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les 6; Conser
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           H(+)(Out).
SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONEN
CORE - AND CF(0) - THE MEMBRANE PROTON
                                                                 FUNCTION: KEY COMPONENT OF THE PROTON CHANNEL; IT MEDIRECT ROLE IN THE TRANSLOCATION OF PROTONS ACROSS CATALYTIC ACTIVITY: ATP + H(2)0 + H(+)(In) = ADP +
                                                                                                                                                                                                                                                                                                                                                                            6803
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LLLVIA 14
                                                                                                                                                                                                                                                                                                                                                         Mol.
                                                                                                                             3:109-136(1996)
                                                                                                                                                                                                                                                                                                                                                                                                               Nelson N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          granulovirus).
                                                                                                                                                                                                                                                                                                                                                          Biol.
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                                                                                                                                                                                                                                                                                                                                                     17:641-652(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=1832989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18556 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       no RNA stage; Baculoviridae; Granulovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
               HAVE 2 COMPONENTS, CF(1) TH
MEMBRANE PROTON CHANNEL. CF(1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 24;
Pred. No.
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GAMMA(1), DELTA(1),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synechocystis
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                 THE CATALYTIC (1) HAS FIVE
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                                                                                         THE MEMBRANE
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Best Local
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                                                                                                                                                                                                                                                                                                                             SUR4_CAEEL STANDARD; PRT Q18804; O18006; O1-NOV-1997 (Rel. 35, Created) O1-NOV-1997 (Rel. 35, Last sequent 15-UIL-1999 (Rel. 38, Last annotal Surfeit locus protein 4 homolog. SURF-4 OR C54H2.5.
                                                                                                                                                                                                                                                                                                                                                                                                                         _CAEEL
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TRANSMEM
                                                                           Fulton L., Gattung S.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
-!- SUBCELLULAR LOCATION: Integral membrane protein. Encreticulum (By similarity).
-!- SIMILARITY: BELONGS TO THE SURF4 FAMILY.
                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X58128; CAA41130.1; -. EMBL; D90900; BAA16740.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
 between the Swiss Institute of Bloinforthe European Bioinformatics Institute use by non-profit institutions as lamodified and this statement is not remo
                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                          STRAIN=Bristol N2;
                                                                                                                                                                                               genomes
                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                         SEQUENCE FROM
                                                                                                                                                                                                                        Armes N.,
                                                                                                                                                                                                                                      MEDLINE=96413309;
                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                            "Surfeit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; D90900; BAA16740.1; -. S17746; PWYBAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAS THREE MAIN SUBUNITS: A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      yen ion transport; CF(0); Transmembrane; Complete proteome.

MEM 27 44 POTENTIAL.

TEM 63 82 POTENTIAL.

SM 122 140 POTENTIAL.

SM 160 179 POTENTIAL.

4 225 242

247
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s; TIGR01131; ATP_synt_6_or_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 6; Conserv
                                                                                                                                                                                                         Locus gene
                                                                                                                                                                                                                                               FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                          Fried M
                                                                                                                                                                                    Biol.
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                                                                                                                                                                                  16:5591-5596(1996)
                                                                                                                                                                                                                                      PubMed=8816471
                                                                                                                                                                                                         homologs are widely distributed in invertebrate
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Pred. No.
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                                     Bioinformatics
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            long
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            There are no rest
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  Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                                                                                                      Endoplasmic
                           restrictions
    and
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                                                                                                                                                                                                                                             STRAIN-ATCC 15692 / PAO1;

MEDLINE-20437337; PubMed-10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

RA Garber R.L., Golltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

RA Raizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa FAO1, an

"Opportunistic pathogen.";

"AL Nature 406:959-964(2000);

"I Nature 406:959-964(2000);

"C -! CATALYTIC ACTIVITY: Cleavage of N-terminal leader sequences from

"C SECTELGULAR LOCATION: Type II membrane protein. Inner membrane.

"I FADER DEFETIOASE FAMILY S26; ALSC KNOWN AS TYPE
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Best Local
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                                        the European Bioinformatics Institute of Bioinformat use by non-profit institutions as long modified and this Statement is not removed. entitles requires a license agreement 'or send an email to 'license agreement'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                091567;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Signal peptidase I (EC 3.4.21.89) (Spase I) (
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    EMBL;
                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas aeruginosa.
Bacteria; Proteobacteria; gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WormPep; C54H2.5; CE06987.
InterPro; IPR002995; Surf4.
Pfam; PF02077; SURF4; 1.
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Prodom; PD010195; Surf4; 1.
PROSITE; PS01339; SURF4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U58728; AAB00591.1; -. EMBL; Y14949; CAA75173.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas
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                                                                                                                                                                                                                                 I LEADER PEPTIDASE FAMILY.
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    AE004511; AAG04157.1;
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A -> R (IN REF. 1).
8FF2848676CC0245 CRC64;
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                                                                    (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 2e+02;
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      InterPro; IPR000508; SigpTase.
InterPro; IPR000223; SigPTase_S26A.
InterPro; IPR000223; SigPTase_S26A.
InterPro; IPR000223; SigPTase_S26A.
InterPro; IPR000227; LEADERPTASE.
PR01TS; PR007501; SPASE_I_1; 1.
PR0SITE; PS00760; SPASE_I_2; 1.
PR0SITE; PS00761; SPASE_I_3; 1.
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DOMAIN
                                                                                                                                                           modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBE the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                            secreted and periplasmic proteins precursor.
-i- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S26; ALSO KNOWN AS TYPE
                                                                                                                                                                                                                                                                                                               MEDLINE=92189595; PubMed=1546969;
Black M.T., Munn J.G.R., Allsop A.E.;
"On the cattalytic mechanism of prokaryotic leader peptidase 1.";
Biochem. J. 282:539-543(1992).
-i- CATALYTIC ACTIVITY; Cleavage of N-terminal leader sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEPB.
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01-NOV-1995 (Rel.
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PROSITE; PS00501, SPASE I_1; 1.
PROSITE; PS00760; SPASE I_2; 1.
PROSITE; PS00761; SPASE I_3; 1.
Inner membrane; Transmembrane;
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InterPro; IPR000223; SigPTase_S26A.
Pfam; PF00461; Peptidase_S26; 1.
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-NCIMB 10586;
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                                                                                                                        PIR; S22414; S22414.
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6; Conser
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I (EC 3.4.21.89) (SPase I) (Leader peptidase
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Pred. No.
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Transmembrane;

Hydrolase; Protease.

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Pfam; PF01566; Nramp; 1.
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Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
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                                                  TRANSMEM
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Mol. Microbiol. 28:403-412(1998).
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SUBCELLULAR LOCATION: Integral membrane
SIMILARITY: BELONGS TO THE NRAMP FAMILY.
                                                                                                                                                                                                                                                                             European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                FUNCTION: H(+)-STIMULATED, HIGHLY SELECTIVE, MANGANESE UPTAKE
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(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
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Pred. No. 2.1e+02;
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                    A006ECFAFE3F0DB0 CRC64;
                                                                                                                                                          Transmembrane.
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Length 415;
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Matches 6; Conserv
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., H
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Badcock K., Basham D., Brown D., Chillingworth T., Moule S., Murphy
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable manganese transport protein mntH (BRAMP).
MNTH OR RV0924C OR MT0951 OR MTCY2IC12.18C.
 TRANSMEM TRANSMEM
                                                                                                                                                                                                                                 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         005916;
                                                                                                                                                                        EMBL; AE006981; AAK45198.1; TIGR; MT0951; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (APR-2001) to the
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                                                    Transport;
                                                                                                                   Pfam; PF01566; Nramp;
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                                   TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         laboratory strains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Whole genome comparison of Mycobacterium tuberculosis clinical and
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                                            HOFB_HAEIN STANDARD; PRT; 464 AA. P44622; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P51363;
01-OCT-1996
01-OCT-1996
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                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
            Bacteria;
                    Protein transport protein hofB HOFB OR HOPB OR HI0298. Haemophilus influenzae.
                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                           Chloroplast; Hypothetical protein.
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SIMILARITY: BELONGS TO THE YCF44 FAMILY.
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           Proteobacteria;
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kDa protein ycf44 (ORF437).
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          subdivision; Pasteurellaceae;
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P50747; Q99451;
01-OCT-1996 (Rel. 34, Created)
101-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Biottin--protein ligase (EC 6.3.4.-) (Biottin apo-protein ligase)
[Includes: Biotin--(methylmalonyl-CoA-carboxyltransferase] ligase
(EC 6.3.4.9); Biotin--(propionyl-CoA-carboxylase (ATP-hydrolyzing]]
ligase (EC 6.3.4.10) (Holocarboxylase synthetase) (HCS);
Biottin--(methylcrotonoyl-CoA-carboxylase) ligase (EC 6.3.4.11);
Biottin--[acetyl-CoA-carboxylase] ligase (EC 6.3.4.11);
             Niikawa N., Matsubara Y., Narisawa "Isolation and characterization of holocarboxylase synthetase cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
                                                                                           TISSUE=Liver;
MEDLINE=95144167;
                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae. NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00437; GSPII_E; 1.

ProDom; PD000739; GSPII_E; 1.

PROSITE; PS00662; T2SP_E; 1.

PROSITE; PS00662; T2SP_E; 1.

Transport; ATP-binding; Complete proteome.

NP_BIND 264 271 ATP (POTENTIAL).

SEQUENCE 464 AA; 52983 MW; 4923156BE45BD6A2
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holocarboxylase synthetase c
Nat. Genet. 8:122-128(1994).
                                                                          Suzuki Y., Aoki Y.,
                                                                                                                                SEQUENCE FROM N.A., AND VARIANT HCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U32715; AAC21962.1; -. TIGR; HI0298; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rd.";
Science 269:496-512(1995).
... STMTLARITY: BELONGS TO THE PULE/OUTE/EXEE/XPSE/XCPR FAMILY.
                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
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STRAIN=Rd / KW20 / ATCC 51907;
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Pred. No. 3.1e+02;
Mismatches 0;
                                                                      Chiba Y., Iwamatsu A., Kishino
                                     mutations in
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RA Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A RA Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D., Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W., & Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S., & Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E., & Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P., & Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H. & Ramser J., Beck A., Klages S., Hennig S., Riesselmann I., Dagand E., & Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F., The DNA sequence of human chromosome 21.";
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SEQUENCE FROM N.A.
Ohira M., Seki N., N
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[7]
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                                                                                 MEDLINE=90*1491...
Dupuis I., Leon-Del-Rio A., Leclerc D., Cumpul.
Saudubray J.M., Herman G., Gibson K.M., Gravel R.A.;
"Clustering of mutations in the biotin-binding region of
"Clustering of mutations in the biotin-responsive multiple"
                                                                                                                                                                                                                                                        Aoki Y., Suzuki Y., Sakamoto O., Li X., Takahashi K., Chtake J. Sakuta R., Ohura T., Miyabayashi S., Narisawa K.; "Molecular analysis of holocarboxylase synthetase deficiency: missense mutation and a single base deletion are predominant:
                                                                                                                                                                                                                                                                                                                                                                                                                                 Dahmane N., Ait Ghezala G., Gosset P., Chamoun Z.,
Dufresne-Zacharia M.C., Lopes C., Rabatel N., Gassanova-Maugenre
Chettouh Z., Abramowski V., Fayet E., Yaspo M.L., Korn B.,
Blouin J.L., Lehrach H., Poustka A., Antonarakis S.E., Sinet P.M.
Creau N., Delabar J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        spectrum of
Hum. Genet.
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"Structure of human holocarboxylase synthetase gene and mutation
"Structure of holocarboxylase synthetase deficiency.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shintani A., Asakawa S., Shimizu N.; "Genomic sequencing of 1.2-Mb region on human Submitted (NOV-1999) to the EMBL/GenBank/DDBJ
                   MEDLINE=98057254;
                                                                                                                                                                                         VARIANT HCS ASN-571
                                                                                                                                                                                                                                                                                                                                                                                               "Transcriptional map of the involved in down syndrome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-92 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hattori M., Fujiyama A., Taylor T.D., Watane Park H.-S., Toyoda A., Ishii K., Totoki Y.,
                                     VARIANTS
                                                                                                                                                                                                                                                                                                                              MEDLINE=96125714; PubMed=8541348;
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Taheri S., Christensen E
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Biophys. Acta 1272:168-174
                                  HCS PRO-237 AND MET-550
                                                                                                                                                                                                                                                                                                                                                                                    48:12-23(1998).
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                                                                    Genet.
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                                                                    5:1011-1016(1996).
                   PubMed=9396568;
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Y., Eki T., Murakami Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AND VARIANTS HCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minoshima
                                                                                                                                                                                                                         1272:168-174(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sakamoto
 Sakamoto
                                                                                                                                                                                                                                                                                                                                                                                                                     2.5-Mb CBR-ERG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O., Hlrausum., Ohira
..., Kubota M., Ohira
... Asaki
 0.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kawasaki K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Watanabe H., Yada
 Chikaoka H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nomura N., Oh
Y., Saito T.,
                                                                                                                                                                                                                                                                                                                                                                                                                   region of chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W-508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chromosome databases.
                                                                                                    multiple carboxylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nakatoh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M-550 AND
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a M.,
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                                                                                                                                                       Sweetman
 Takita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       )hara O.,
];chikawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                   B.,
Sinet P.M.,
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S
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                                                                                                                                                                                                                                                                                                            Α.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S-581
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Hum. Genet. 104:143-148(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              biotin was not elevated in a patient with Pediatr. Res. 42:849-854(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99204600;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'Characterization of mutant holocarboxylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Cytoplasmic and mitochondrial.

SUBCELLULAR LOCATION: Cytoplasmic and mitochondrial.

TISSUE SPECIFICITY: MOSTLY EXPRESSED IN MUSCLE, PLACENTA, IN

LESSER EXPRENT IN THE BRAIN, KIDNEY, PANCREAS, LIVER AND LUNG.

DISEASE: DEFECTS IN HLCS ARE THE CAUSE OF HOLOCARBOXYLASE

SYMPHETASE DEFICIENCY (HCS) (OR BIOTIN RESPONSIVE MULTIPLE

CARBOXYLASE DEFICIENCY), AN AUTOSOMAL RECESSIVE DISORDER

CHARACTERIZED BY METABOLIC KETOACIDOSIS, HYPERAMMONEMIA, EXCRETION

OF ABNORMAL ORGANIC ACID METABOLITES, AND DERMATITIS. CLINICAL AND

BIOLOCHEMICAL SYMPTOMS IMPROVE DRAMATICALLY WITH ADMINISTRATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COA:carbon-dioxide ligase (ADP-forming)].

CATALYTIC ACTIVITY: ATP + blotin + apo-[3-methylcrotonoyl-COA:carbon-dioxide ligase (ADP-forming)] = AMP + diphosphate + [3-methylcrotonoyl-COA:carbon-dioxide ligase (ADP-forming)].

CATALYTIC ACTIVITY: ATP + blotin + apo-[acetyl-COA:carbon-dioxide ligase (ADP forming)] = AMP + diphosphate + [acetyl-COA:carbon-dioxide ligase (ADP forming)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BIOTIN.
SIMILARITY: WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COA:pyruvate carboxyltransferase].

CATALYTIC ACTIVITY: ATP + biotin + apo-[propanoyl-CoA:carbon-diaxide ligase (ADP-forming)] = AMP + diphosphate + [propanoyl-CoA:carbon-diaxide ligase (ADP-formi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTACHMENT OF BIOTIN. ACTS ON VARIOUS CARBOXYLASES SUCH AS ACETYL-COA-CARBOXYLASE, PYRUVATE CARBOXYLASE, PROPIONYL COA CARBOXYLASE, AND 3-METHYLCROTYONYL COA CARBOXYLASE.

CATALYTIC ACTIVITY: ATP + biotin + apo-[methylmalonyl-CoA:pyruvate carboxyltransferase] = AMP + diphosphate + [methylmalonyl-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: POSTTRANSLATIONAL MODIFICATION OF SPECIFIC PROTEIN ATTACHMENT OF BIOTIN. ACTS ON VARIOUS CARBOXYLASES SUCH AS AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIGASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLU-333; ILE-462; ASN-571; 04600; PubMed=10190325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E.COLI BIRA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER
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HCS deficiency.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUKARYOTIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BIOTIN--PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Narisawa
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MIM;
                                                              Pfam; PF02237; BPL_C; 1
Pfam; PF03099; BPL_LipA
                                                                                InterPro; IPR003142; BPL_C.
InterPro; IPR004143; BPL_LipA_LipB
InterPro; IPR004408; BirA_ligase.
                                                                                                                              Genew;
                                                                                                                                                                                                                                  EMBL; D23672;
                   ; Multifunctional e
.R 563 609
MT 237 237
                                                                                                                            HGNC:4976; HLCS
                                        TIGR00121; birA_ligase; 1.
ultifunctional enzyme; Disease mutation
  333
                                                                                                                                                                                                                                  BAA04902.1;
                                                               LipA_LipB;
                                                                                                                                     JOINED.
JOINED.
-.
SOME, TO AVIDIN.
L -> P (IN HCS).
/FTId=VAR_005084.
V -> E (IN HCS; <
                             SOME,
  <10% ACTIVITY)
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0;

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RESULT 15
CHS5_USTMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 6; Conserv
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Chitin synthase 5 (EC 2.4.1.16) (Chitin-UDP acetyl-glucosaminyl transferase 5) (Class-IV chitin synthase 5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
SEQUENCE
                                    Transferase; Glycosyltransferase; Transmembrane; Cell wall; Multigene family.
                                                           Interpro; IPR004835; Fungi_chitin_syn.
Interpro; IPR001173; Glycos_transf_2.
pfam; PF03142; Chitin_synth_2; 1.
                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                        Ustilago maydis (Smut fungus).
Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
NCBI_TaxID-5270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHS5_USTMA
O13394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT
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                                                                                                 EMBL; AF030553; AAB84284.1; -
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                                                                                                                                                                                                                                                                                                                             maydis."
                                                                                                                                                                                                                                                                                                                                                   Xoconostle-Cazares B., Ruiz-Herrera J.;
                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-518
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-98123008; PubMed-9454647;
                                                                                                                                                                                                                                                                                                                                      "Umchs5, a gene coding for a class IV chitin synthase in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215 LLLVIA 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LLLVIA 6
                                                                                                                                                                                                                                   glucosaminyl)}(N+1).
SUBCELLULAR LOCATION: Plasma membrane-bound.
SIMILARITY: BELONGS TO THE CHITIN SYNTHASE FAMILY. SUBFAMILY CLASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               558
726 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; ilarity 100.0%; Conservative 0
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                        AA;
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                        137291 MW;
 100.0%;
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V -> M (IN HCS).
/FTId=VAR_009198.
D -> N (IN HCS; ALM
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E -> K (IN DET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G -> S (IN HCS; <10% ACTIVITY).
/FTIG=VAR_009200.
MISSING (IN HCS; 14% OF ACTIVITY).
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Pred. No. 4.4e+02;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /FTId=VAR_009197.
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Score 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                855B8E52106D675F CRC64;
                        02A91C8C6B1CBB2D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1239
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DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <10% ACTIVITY).
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Length 1239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                        Ustilago
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Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps
Qy 1 LLLVIA 6
| | | | | | | | |
Db 709 LLLVIA 714
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Search completed: January 3, 2003, 15:29:21 Job time: 6.18182 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
                                                                                                                                                                                                                                                                                            Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                         number of hits satisfying chosen parameters:
SPTREMBL_21:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fung1:*
4: sp_human:*
5: sp_invertebrate
6: sp_manmal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_blage:*
10: sp_plage:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:
14: sp_unclassifie
15: sp_bacteriap:*
17: sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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sp_archeap:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

16	15	14	13	12	11	10	9	œ	7	o	ъ	4	ω	2	دبو	Result No.
24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	Score
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Q8UAB6	Q8ZDP9	P72696	085820	Q9ZBX3	091СВ9	044086	Q8WET9	Q9MIU4	Q9SIE7	Q8TWZ8	Q9PGB9	Q9NIQ2	Q8XPU9	Q9NIQ1	Q9DGL8	ID
		P72696 synechocyst	085820 actinobacil	Q9zbx3 streptomyce	Q9ycb9 aeropyrum p	044086 caenorhabdi	Q8wet9 lyonsia hya	Q9miu4 hyphochytri	Q9sie7 arabidopsis	Q8twz8 methanopyru	Q9pgb9 xylella fas	29niq2 trypanosoma	Q8xpu9 ralstonia s	29niq1 trypanosoma	Q9dgl8 gallus gall	Description

	45	44	43	42	41	40	39	38	37	36	35	34	3 3	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
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•	Q9epe8 mus musculu	O54201 streptomyce	Q8s0a9 oryza sativ	Q9be74 macaca fasc	Q9k5q7 bacillus ha	Q930c1 rhizobium m	Q40025 hordeum vul	Q98m07 rhizobium l	067873 aquifex aeo	Q9jrm9 actinobacil	Q9a164 streptococc	Q8rgf7 fusobacteri	Q9euu4 pseudomonas	Q9ak38 streptomyce		067832 aquifex aeo			Q9ybp9 aeropyrum p	064468 arabidopsis	Q9zcd2 rickettsia	Q8vf60 mus musculu	016463 caenorhabdi	o	Q9f0g9 pseudomonas		Q8ug43 agrobacteri	P74131 synechocyst	Q9ug33 homo sapien

# ALIGNMENTS

RESULT Q9NIQ1 ID Q AC Q DT 0 DT 0 DT 0	Ae Ma Qy Db	RT RT SQ	R R R R R C C C	OC O O DE	RESULT Q9DGL8 ID Q AC Q DT O DT O DT O
IT 2 Q9NIQ1 PRELIMINARY; PRT; 107 AA. Q9NIQ1: 01-OCT-2000 (TrEMBLrel. 15, Created) 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)	Hest Local Similarity 100.0%; Pred. No. 1.8e+02; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  1 LLIVIA 6                9 LLIVIA 14	ion of genes (JUL-2000) 85876; AAGOO 98 AA; 11	GAILUS.  NCBI_TAXID=9031;  [1]  [1]  SEQUENCE FROM N.A.  SEQUENCEFIBROBLAST;  Hartl M., Bister K.;	sed chemokine. us (Chicken). Metazoa; Chordata ; Aves; Neognatha	LT 1 (A) OPDGL8 PRELIMINARY; PRT; 98 AA. OPDGL8; O1-MAR-2001 (TIEMBLIEL 16, Circated) O1-MAR-2001 (TIEMBLIEL 16, Last sequence update) O1-MAR-2001 (TIEMBLIEL 16, Last annotation update)

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O9NIQ2;
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01-OCT-2000 (TrEMBLrel. 1:
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                                                                                                                                                                                                                                                     "Genome sequence of the plant pathogen Ralstonia solanacearum."; Nature 415:497-502(2002).
EMBL; AL646085; CAD18688.1; -.
Plasmid; Complete proteome.
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01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
 Mucin-like
                                                                                                                                                                                                                                           SEQUENCE
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01-MAR-2002
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D1 Noia J.M., D'Orso I., Sanchez D.O., Frasch A.C.;
D1 Noia J.M., D'Orso I., Sanchez D.O., Frasch A.C.;
"AU-rich elements in the 3'-untranslated region of a new m
gene family of trypanosoma cruzi confers mRNA instability
modulates translation efficiency.";
J. Biol. Chem. 275:10218 -10227 (2000).
EMBL; AF203096; AAF67333.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
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NCBI_TaxID=5693;
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J. Biol. Chem. 275:10218-10227(2000).

EMBL. AF203095; AAF67332.1; -.
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MEDLINE=20209394;
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NCBI_TaxID=5693;
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"AU-rich elements in the 3'-untranslated region of a new mucin·type
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Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D., Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S., Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M., Venter J.C.;
"Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N., Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L., Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O., Malykh A.G., Koonin E.V., Kozyavkin S.A.;

"The complete genome of hyperthermophile Methanopyrus kandleri AV19 and monophyly of archaeal methanogens."

proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seg
01-MAR-2002 (TrEMBLrel. 20, Last ann
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                                                                                                                                                                                                              STRAIN=CV. COLUMBIA;
MEDLINE=20083487; PubMed=10617197;
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01-MAY-2000
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MEDLINE=21927647; PubMed=11930014;
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Q9MIU4;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 21, Last annotation updat
                                                                                           OBWET9 PRELIMINARY; PRT; 223 AA.
OBWET9; PREMBLrel 20, Created)
Ol-MAR-2002 (TrEMBLrel 20, Last sequence up
Ol-JUN-2002 (TrEMBLrel 21, Last annotation
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Pfam; PF02790; COX2_TM; 1.
PRINTS; PR01166; CYCOXIDASEII
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"A cytochrome c oxidase II molecular phylogeny
Peronosporomycetes (Comycetes).";
Mycologia 92:674-68 (2000).
EMBL; AF086701; AAF80243.1; -
InterPro; IPR001505; Copper_CuA.
InterPro; IPR002429; Cyt_c_ox_2.
                                                          Cytochrome oxidase
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NCBI_TaxID=42384;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 3.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D28BD3E4A7A73B67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B0322292368BB92D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                   sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A
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                                                                                                  update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0f
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 193;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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044086;
01-JUN-1998 (TrembLrel. 0
01-JUN-1998 (TrembLrel. 0
01-JUN-2002 (TrembLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               st Local satches
                                                                                                                                                                                                           Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Couper J., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., McMurray A., Morthore B., O'Callaghan M.,
Parsons J., Percy C., Rikken L., Roopra A., Saunders D., Shownkeen
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vauphan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

Giribet G., Wheeler W.C.;

Giribet G., wheeler W.C.;
Submitted (SEP-1997) to the EMBL; AF022977; AABB8611.1; InterPro; IPR001611; LRR. Cte InterPro; IPR000372; LRR_Nte
                                                                Waterston R.;
                                                                             STRAIN-BRISTOL N2;
                                                                                          SEQUENCE FROM N.A.
                                                                                                                                 "The
                                                                                                                                               Davidson S., Wohldmann P.;
                                                                                                                                                           STRAIN-BRISTOL
                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                  Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                       STRAIN=BRISTOL N2;
MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZK994.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZK994.4 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00115; COX1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JAN-1999) to the EMBL; AF120654; AAL55504.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "On bivalve phylogeny: a high-level phylogeny of the mollusk class Bivalvia based on a combined analysis of morphology and DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Mollusca; Bivalvia; Anomalodesmata; Pholadomyoida;
Pandoroidea; Lyonsiidae; Lyonsia.
NCBI_TaxID=120442;
[1]
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                                                                                                                  sequence of C. elegans tted (DEC-1997) to the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR000883; COX1.
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223 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                              N2;
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LRR_Nterm
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             LRR_Cterm
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21,
                                                  EMBL/GenBank/DDBJ databases
                                                                                                                   cosmid ZK994.";
EMBL/GenBank/DDBJ databases.
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Last annotation update)
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Pred. No.
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3.7e+02;
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Pfam; PF00166; LRRCT; 1.
Pfam; PF01463; LRRCT; 1.
Pfam; PF01462; LRRWT; 1.
SMART; SM000370; LRR; 3.
SMART; SM00082; LRRCT; 1.
SMART; SM00013; LRRCT; 1.
SMART; SM00013; LRRCT; 1.
SMART; SM00013; LRRCT; 1.
                                                                                                                                  Q9ZBX3;
Q9ZBX3;
Q1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
Q1-MAY-1999 (TrEMBLrel. 21, Last annotation update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9YCB9;
01-NOV-1999
01-NOV-1999
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AP000061; BAA80329.1; -. Hypothetical protein; Complete SEQUENCE 232 AA; 24673 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Res. 6:83-101(1999)
                                                                                                       Bacteria; Firmicutes;
                                                                                                                           Streptomyces coelicolor
                                                                                                                                                                                                                                                                               Q9ZBX3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-K1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Desulfurococcaceae;
NCBI_TaxID=56636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Archaea;
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                   SEQUENCE FROM N.A
                                                             NCBI_TaxID=1902;
                                                                                 Actinomycetales;
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                                                                                                                                                                                                                                                                                                                                                                                       82 LLLVIA 87
                                                                                                                                                                                                                                                                                                                                                                                                                          1 LLLVIA 6
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ilarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                                             PRELIMINARY;
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llarity 100.0%;
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                                                                                 Streptomycineae;
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                                                                                                       Actinobacteria;
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Pred. No. 3.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 24; DB 17;
Pred. No. 3.9e+02;
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E8ECBF8BF27691A0 CRC64;
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                                                                                 Streptomycetaceae;
                                                                                                                                                                                                                                                                             239
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                                                                                                       Actinobacteridae;
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                                                                                 Streptomyces
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RESULT 14
P72696
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O8582
ID 08582
AC 08582
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AC 01-N0
DT 01-N0
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P72696;
P72696;
01-FEB-1997
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085820;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Winston J.L., Sezate S.A., Dyer D.W., McLaughlin R.E.; "Demonstration of a polyamine requirement for growth of Actinobacillus actinomycetemcomitans, and identification of the putative polyamine transport operon."; Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genome sequence of coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL; AL034355; CAA22231.1;
                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                    Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00528; BPD_transp; 1.
PROSITE; PS00402; BPD_TRANSP_INN_MEMBR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-Y4;
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Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Actinobacillus actinomycetemcomitans (Haemophilus
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(TrEMBLrel. 02,
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                                                                                                                                                                                                                                                                                                                                          Transport. AA; 27390 MW;
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Pred. No. 4e+
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Pred. No. 4.1e+02;
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Q8ZDP9;
Q8ZDP9;
Q8ZDP9;
Q1-MAR-2002 (TrEMBLrel. 20, Cr
Q1-MAR-2002 (TrEMBLrel. 21, Lr
Q1-JUN-2002 (TrEMBLrel. 21, Lr
                                                                            Query Match
Best Local
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STRAIN=CO-92 / BIOVAR ORIENTALIS;
MEDLINE=21470413; Pubmed=11586360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis NCBI_TaxID=1148;
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                                                                                                                         InterPro; IPR000620; DUF6.
Pfam; PF00892; DUF6; 1.
Hypothetical protein; Complete
SEQUENCE 295 AA; 30755 MW;
                                                                                                                                                                                                                                   Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G
                                                                                                                                                                                                                                                                                  Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L., Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M. Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D90900; BAA16703.1; -. Hypothetical protein; Complete SEQUENCE 281 AA; 31695 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
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                                                                                                                                                                                                       "Genome sequence of Yersinia pestis, the Nature 413:523-527(2001).
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Pred. No. 4.8e+02;
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Listing first 45 summaries
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
                                                                                                  /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
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Compugen Ltd.
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18-OCT-2001.

05-APR-2001;

2001WO-US11150

WPI; 2002-061944/08

Hammond DJ, Wiltshire VR,

Carbonell R,

Shen Ή 05-APR-2000; 2000US-0543188

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TECHNOLOGIES INC

Result No.	Score	1	ength	₽ .	ID	Description
₽	34		6	23	AAU11844	Peptide ligand for
2	32	94.1	49	22	AAE10210	Human bone marrow
ω	32	94.1	79	21	AAG06438	Arabidopsis thalia
4	32	94.1	79	21	AAG24460	Arabidopsis thalia
5	32	94.1	79	21	AAG35187	Zea mays protein f
6	32	94.1	79	21	AAG35298	Zea mays protein f
7	32	94.1	88	21	AAG06437	Arabidopsis thalia
8	32	94.1	88	21	AAG24459	Arabidopsis thalia
9	32	94.1	88	21	AAG35186	Zea mays protein f
10	32	94.1	88	21	AAG35297	Zea mays protein f

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ALIGNMENTS	ABG60099 AAG35185 ABG30281 AAG35185 ABG30281 AAG03171 AABG1777 AAR114458 AAG17986 AAG17987	3 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
	Human Dilire polype Human Dilire polype Human Dilire polype Rovel human diagno Novel human diagno Novel human secreted pro Human secreted pro Human secreted pro Human secreted pro Arabidopsis thalia Propionibacterium Arabidopsis thalia Propionibacterium Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Streptococcus poly S. agalactiae extr Novel human diagno Novel human secrete Human apene 10 enco Human apene 10 enco Human secrete Drosophila melanog Glycerol-3-phospha Klebsiella pneumon Cytosolic glycerol Cytosolic glycerol Saccharomyces cere Human G-protein co Human mutant G pro	71910

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RESULT 1
AAU11844
                                                                                                                                                                                                          Prion protein; Prp; ligand; octapeptide motif; scrapie; prion-associated disease; Creutzfeldt-Jakob disease; Gerstmann-Straussler-Scheinker disease; fatal familial insomnia;
                                                                                                                                                 feline spongiform encephalopathy; bovine spongiform encephalopathy; transmissible mink encephalopathy; exotic ungulate encephalopathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU11844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU11844 standard; peptide; 6 AA
WO200177687-A2.
                                                            Synthetic.
                                                                                                                        chronic wasting
                                                                                                                                                                                                                                                                                                                                   Peptide ligand for Prion protein, PrP, #19
                                                                                                                                                                                                                                                                                                                                                                                                  26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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RESULT 2
AAE10210
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Best Local :
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              Isolated polynucleotide encoding bone marrow derived polypeptides useful for treating, e.g., Parkinson's, Alzheimer's, cancer, arth Crohn's disease, and inflammatory bowel disease
                                                                                                                                                                                                       07-MAR-2000; 2000US-0519705
19-MAY-2000; 2000US-0574454
14-JUL-2000; 2000US-0616847
30-NOV-2000; 2000US-0250583
                                                                                                                                                                                                                                                                                                                                                                                                             stem cell growth; haematopolesis regulation; immunoregulatory; anaemia; Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis; infection; HIV; malaria; fungal; cancer; autoimmune disorder; arthritis; Crohn's disease; inflammatory bowel disease; leukaemia; gene therapy.
                                                                                WPI; 2001-565565/63.
N-PSDB; AAD17391.
                                                                                                                                            Ford JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              scrapie, bovine or feline spongiform encephalopathy, transmissible mink or exotic ungulate encephalopathy, or chronic wasting disease. The present sequence is a ligand of the invention.
                                                                                                                                                                                                                                                                                     07-MAR-2001; 2001WO-US07274
                                                                                                                                                                                                                                                                                                                        13-SEP-2001
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                                                                                                                                                                           (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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1 IQIWIF 6
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les 6; Conserv
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Pred. No.
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                                  arthritis
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RESULT 3
AAG06438
     PARRAR RARAR                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ωy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to novel human bone marrow polynucleotides and polypeptides. The polypeptides of the invention may exhibit various activities e.g. cytokine and cell proliferation/differentiation, considered the constant of the invention and immune stimulation/consuperssion. The polynucleotides are polypeptides of the invention may be used to detect bone marrow cells, for treating, e.g., Parkinson's confections such as HIV, malaria and fungal infections, cancer, autoimmune disorders, arthritis, Crohn's disease, inflammatory bowel disease, and considered as arthritis, crohn's disease, inflammatory bowel disease, and considered as a markers for tissues in which the corresponding protein is preferentially expressed; as molecular weight markers and as probes to hybridise and discover novel, related DNA consumences. The polypucture may be used in assays to determine biological activity, to raise antibodies or illicit an immune response and as a creagent in assays. The present sequence is a human bone marrow derived
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Best Local
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                  09-MAR-1999
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01-APR-1999
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08-APR-1999
116-APR-1999
116-APR-1999
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04-MAY-1999
05-MAY-1999
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99US-013077
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99US-0131449
99US-0132407
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99US-0126785
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Pred. No.
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64;
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RESULT 4
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| IQIWLF 23
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990S-0128714

990S-0128714

990S-0130510

990S-0130449

990S-0130449

990S-0130449

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28-OCT-1999;
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netic mapping; gene expression control; orn.  1439.  1439.  1825.  1826.  3180.  3588.  6284.  6284.  6284.  6286.  444.  6286.  4487.  2487.  2487.  2528.	94.1%; Score 32; DB 21; Length arity 83.3%; Pred. No. 1e+02; Onservative 1; Mismatches 0; Inde 3  3  dard; Protein; 79 AA.  (first entry) (first entry) ein fragment SEQ ID NO: 43098.
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21-MAY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                AAG24459 standard;
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                                                                                         Similarity 83.3
5; Conservative
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990S-0149923

990S-0151065

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990S-0160814

990S-0161369

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9905-01231825. 9905-0123548 9905-0125248 9905-0126254 9905-0126254 9905-0126254 9905-0126254 9905-0126254 9905-0126254 9905-012635 9905-012644 9905-012644 9905-012644 9905-012644 9905-012644 9905-012644 9905-012644 9905-012644 9905-012644 9905-012644 9905-012644 9905-012646 9905-012646 9905-012646 9905-012646 9905-012646 9905-01266 9905-01	00 (first entry) is thallana protein fragment SEQ ID NO: 28138. is thallana protein fragment SEQ ID NO: 28138. dentification; signal transduction pathway; metabolic pathway; tion assay; genetic mapping; gene expression control; promoter; on sequence. is thallanaA2. 00. 00; 2000EP-0301439.
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J. 35186
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DE Zea mays r
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31-AUG-1999
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11-OCT-1999
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990S-0151080.
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990S-01593.
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83.3%;
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Pred. No. 1.1e+02;
1; Mismatches 0;
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promoter;
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99US-0155659. 99US-0156458. 99US-0156596. 99US-0157117.

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08-OCT-1999;
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                                                                                       WO200220754 - A2
                                                                                                                                       Homo sapiens
29-AUG-2001; 2001WO-US27127.
                                               14-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                            Human DITHP polypeptide #155
                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG60097 standard; Protein; 101 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 IQIWIF 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IQIWLF 32
                                                                                                                                                                                                          gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9908-0159330
9908-015931
9908-0159637
9908-0159638
9908-0160761
9908-0160768
9908-0160768
9908-0160815
9908-0160815
9908-0160815
9908-0160981
9908-0160981
9908-0161406
9908-0161406
9908-0161406
9908-0161406
9908-0161406
9908-0161406
9908-0161359
9908-0161359
9908-0161359
9908-0161359
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9905-0159294.
9905-0159295.
9905-0159329.
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99US-0158232.
99US-0158369.
                                                                                                                                                                                                  bone marrow; lung; ovary; pancreas; prostate; spleen;
                                                                                                                                                                                                                          disorder; transport disorder; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.1%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 32; [
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 21;
1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                               kidney;
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RESULT 12 ABG60099

XXX

ABG60099

ABG60099 standard; Protein;

110

ΑA

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δõ
     Вb
                                                                                                                                        The invention relates to human diagnostic and therapeutic (dithp)
CC polynucleotides and their associated polypeptides (DITHP polypeptides).
CC The sequences of the invention are used in the treatment and diagnosis of CC cell proliferative disorders (e.g. atherosclerosis, cirrhosis), cancers
CC (e.g. tumours of the adrenal gland, bone, bone marrow, brain, breast, CC cervix, kidney, lung, ovary, pancreas, prostate, skin, spleen, testis or CC thymus), autoimmune/inflammatory disorders (e.g. asthma, bronchitis, psoriasis, osteoporosis), viral infections, bacterial infections, fungal infections, parasitic infections, developmental disorders (e.g. anaemia, CC infections, parasitic infections, developmental disorders (e.g. anaemia, CC epilepsy), seizure disorders (e.g. cerebral palsy, spina bifida), CC endocrine disorders (e.g. thrombosis, aneurysm), metabolic disorders (e.g. obesity, diabetes), neurological disorders (e.g. stroke, amyotrophic lateral sclerosis, multiple sclerosis), gastrointestinal CC amyotropers (e.g. ulcerative colitis, lysinuria) and transport disorders (e.g. myotonic dystrophy, catatonia, peripheral neuropathy). Sequences (e.g. myotonic dystrophy, catatonia, peripheral neuropathy).
                                                                                    Query Match
Best Local
                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-SEP-2000

05-SEP-2000

05-SEP-2000

05-SEP-2000

05-SEP-2000

06-SEP-2000

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Momiyama
Gerstin E
Marwaha R
                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          An isolated polynucleotide useful in diagnostics and therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (INCY-) INCYTE GENOMICS INC.
1 IQIWIF 6
||||:|
40 IQIWLF 45
     40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002-383054/41.
DB; ABK71688.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          29; Page 621; 686pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EH,
                                                                      Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MG,
                                                                                                                                      101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lincoln SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yu JY,
     45
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2000US-229749P.
2000US-229750P.
2000US-229750P.
2000US-230514P.
2000US-230515P.
2000US-230515P.
2000US-230519P.
2000US-230519P.
2000US-230519P.
2000US-230597P.
2000US-230599P.
                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         incoln SE, Altus CM, Dufour GE, Chalup MS, Hillm
u JY, Wright RJ, Gietzen D, Liu TF, Yap PE, Dah
Bradley DL, Rohatgi SD, Harris B, Roseberry AM;
Peralta CH, David MH, Panzer SR, Flores V, Daff
Chen AJ, Chang SC, Au AP, Inman RR;
                                                                                                                                      AΑ;
                                                                                     94.1%;
83.3%;
                                                                    Score 32; DB
Pred. No. 1.3e
1; Mismatches
                                                                                    DB 23;
1.3e+02;
                                                                      0;
                                                                                                   Length 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hillman JL;
                                                                    0;
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                                                                    Gaps
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05-SEP-2000

05-SEP-2000

05-SEP-2000

05-SEP-2000

05-SEP-2000

06-SEP-2000

                  The invention relates to human diagnostic and therapeutic (dithp) polynucleotides and their associated polypeptides (DITHP polypeptides). The sequences of the invention are used in the treatment and diagnosis of cell proliferative disorders (e.g. atherosclerosis, cirrhosis), cancers (e.g. tumours of the adrenal gland, bone, bone marrow, brain, breast, cervix, kidney, lung, ovary, pancreas, prostate, skin, spleen, testis or thymus), autoimmune/inflammatory disorders (e.g. asthma, bronchitis, psoriasis, osteoporosis), viral infections, bacterial infections, fungal infections, parasitic infections, developmental disorders (e.g. anaemia, epilepsy), seizure disorders (e.g. cerebral palsy, spina bifida), endocrine disorders (e.g. thrombosis, aneurysm), metabolic disorders (e.g. obesity, diabetes), neurological disorders (e.g. stroke, amyotrophic lateral sclerosis, multiple sclerosis), gastrointestinal disorders (e.g. stroke, amyotrophic lateral sclerosis, multiple sclerosis), gastrointestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Momiyama
Gerstin E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 endocrine disorder; metabolic disorder; neurological disorder; cervix; gastrointestinal disorder; transport disorder; gene therapy; kidney; addrenal gland; bone marrow; lung; ovary; pancreas; prostate; spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 29; Page 622; 686pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stuart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; DITHP; diagnostic and therapeutic polypeptide; bone; testis; skin cell proliferative disorder; cancer; tumour; autoimmune disorder; brain; inflammatory disorder; viral infection; bacterial infection; seizure; fungal infection; parasitic infections; developmental disorder; breast;
disorders (e.g. ulcerative colitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            An
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (INCY-) INCYTE GENOMICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human DITHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        isolated polynucleotide useful in diagnostics and therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2002-383054/41.
DB; ABK71690.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lincoln SE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-230865P.
2000US-230988P.
2000US-230951P.
2000US-231163P.
2000US-231167P.
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2000US-230519P.
2000US-230595P.
2000US-230597P.
2000US-230598P.
2000US-230599P.
2000US-230599P.
2000US-230610P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bradley DL, Rohat
Peralta CH, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-230515P.
2000US-230517P.
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2000US-230514P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-230583P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Altus CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RJ, Gietzen D, Liu ...
RJ, Gietzen D, Liu ...
Rohatgi SD, Harris B, Rose...
Pavid MH, Panzer SR, Flores V, and transport disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roseberry AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hillman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dahl CR;
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RESULT 13
AAG35185
ID AAG35
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Best Local S
Matches
20-MAY-1999;
21-MAY-1999;
24-MAY-1999;
25-MAY-1999;
27-MAY-1999;
01-JUN-1999;
03-JUN-1999;
                                                                                                                                                                        28-APR-1999;
30-APR-1999;
30-APR-1999;
                                                                                                                                                                                                                                                   23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
01-APR-1999;
06-APR-1999;
                                                                                                                                                04-MAY-1999;
05-MAY-1999;
06-MAY-1999;
                                                                                            14-MAY-1999;
14-MAY-1999;
                                                                                                             11-MAY-1999;
14-MAY-1999;
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07-MAY-1999
                                                                                                                                                                                                 23-APR-1999
23-APR-1999
                                                                                                                                                                                                                  19-APR-1999;
21-APR-1999;
                                                                                                                                                                                                                                            08-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                  hybridisation assay; genetic mapping; gene expression termination sequence; corn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG35185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG35185 standard; Protein; 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (e.g. myotonic dystrophy, catatonia, peripheral neuropathy). Sequence: ABG59943-ABG60220 represent human DITHP polypeptides of the invention
                                                                                                                                                                                                                                                                                                                25-FEB-1999;
                                                                                                                                                                                                                                                                                                                                25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                  Zea mays subsp. mays.
                                                                                                                                                                                                                                                                                                                                                                                                                    Protein identification; signal transduction pathway; metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                     Zea mays protein fragment SEQ
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|QIWLF 62
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5; Conser
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                                                                                                                                                                                                                                                                                                                                2000EP-0301439
                                                                   99US-0132484.
99US-0132485.
99US-0132486.
99US-0132863.
99US-0134218.
99US-0134218.
99US-0134219.
99US-0134721.
99US-0134768.
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99US-0130449.
99US-0130510.
99US-0130891.
99US-0131449.
99US-0132048.
99US-0135124
99US-0135353
99US-0135629
99US-0136021
99US-0136392
99US-0136722
99US-0137722
99US-0137722
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99US-0128234.
99US-0128714.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.1%;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      NO: 42946.
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1.4e+02;
0;
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                                                                                                                                                                                                                                                                                                                                                                                                           promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                    pathway;
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UNN 1999 9918 01318 01318 01 PR 99 - MOS -		************		~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~
	23-Jt 26-Jt 27-Jt 27-Jt 27-Jt 28-Jt 02-At 02-At 04-At 04-At	16-Ju 19-Ju 19-Ju 19-Ju 19-Ju 19-Ju 19-Ju 19-Ju 20-Ju 20-Ju 21-Ju 22-Ju 22-Ju 23-Ju 23-Ju	118-Ju 11	07-J1 08-J1 110-J1 110-J1 116-J1 116-J1 118-J1 118-J1 118-J1 118-J1 118-J1 118-J1
900 01 10 10 10 10 10 10 10 10 10 10 10 1	10-199 16-199 17-199 19-19 19-19 19-19 19-19 19-19 19-19 19-19 19-19 19-19 19-19 19-19 19-19			JUN-19 JUN-19 JUN-19 JUN-19 JUN-19 JUN-19 JUN-19 JUN-19 JUN-19 JUN-19 JUN-19 JUN-19 JUN-19 JUN-19
Column   C				
Column   C	1000 1000 1000 1000 1000 1000 1000 100			
8004.4 8004.5 8005.5 80				
PR 09 AMG 1999 9895 014793 989	5224 5276 5913 5919 5919 5951 5951 6386 6386 6388 7203	4085 4086 4331 4332 4333 4333 44333 44333 4483 4483 5088 5088 5088 51089 5118 5118 5118 5118 5118 5118 5118 51	99463 99763 99763 99899 98999 98999 98999 10991 11287 11287 12803 12903 135977 135977	9453 9453 9453 9453 9453 9453 9453 9453
09-NIG-1999 10-NIG-1999 10-NIG				
09-NIG-1999 10-NIG-1999 10-NIG				
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Homo sapiens

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RESULT 14 ABG29035

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polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymcleotides are also used in diagnostics as expressed sequence tags (I) is useful in gene therapy techniques (I) is useful in gene therapy techniques (I) (II) (II) is useful for generating antibodies against it, detecting or (II), (II) is useful for generating antibodies against it, detecting or (II) and its binding partners are useful in medical indigorations in the polymcleotide suppression or biological activity. (II) and (II) are useful for treating (III) are useful for treating (I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20; SEQ ID No 59394; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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23-AUG-2000; 2000US-0649167
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(I) is useful as hybridisation probes,
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Pred. No.
                                   Mismatches
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                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                         (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                 Sequence
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23-AUG-2000; 2000US-0649167
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Drmanac RT, Liu C,

(HYSE-) HYSEQ INC

N-PSDB;

AAS93222.

WPI; 2001-639362/73.

Query Match
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Matches 5; Conserv

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Sequence

2243 AA

Search completed: January 3, 2003, 15:28:40 Job time : 28.5909 secs В

563 IQIWMF 568

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OM protein - protein search, using sw model
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US-09-543-188A-21
34
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                                                                                                                                                                                                                                                GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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Title:
Perfect score:
Sequence:

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

earched: 283224 seqs, 96134422 residues

al number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	ω	2	بر	No.	Result
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### ALIGNMENTS

1%; Score 33; 3%; Pred. No.	y; translated from GB/EMBL/DDBJ IL> EMBL:ZB1109; PIDN:CAB03254.1; G e: clone R10D12 11 11 13; 240/3 rhabditis hypothetical protein	RESULT 2 T24123 T24123 hypothetical protein R10D12.11 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Jate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change C;Accession: T24123 R;Percy, C. Submitted to the EMBL Data Library, October 1996 A;Reference number: Z10842	Query Match 97.1%; Score 33; DB 2; Best Local Similarity 83.3%; Pred. No. 47; Matches 5; Conservative 1; Mismatches  Qy 1 IQIWIF 6	RESULT 1  C58933  ribosomal protein S3 - Cyanidioschyzon merolae mitochondrion C;Species: mitochondrion Cyanidioschyzon merolae  C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_chan C;Accession: C58933  R;Ohta, N.; Sato, N.; Kuroiwa, T.  Nucleic Acids Res. 26, 5190-3198, 1998  A;Title: Structure and organization of the mitochondrial geno A;Reference number: A58930; MUID:99030526; PMID:9801318  A;Accession: C58933  A;Accession: C58933  A;Status: preliminary  A;Kross-references: D8930; MUID:99030526; PMID:9801318  A;Residues: 1-282 <arn> A;Cross-references: GB:D89861; NID:g4115781; PIDN:BAA36537.1; C;Genetics:  A;Genome: mitochondrion  C;Keywords; mitochondrion</arn>
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R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
                                                                                          probable small nuclear ribonucleoprotein E [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hir. Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: G83831
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Nature 402, 769-777, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    small nuclear ribonucleoprotein homolog [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C;Accession: F85354
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C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
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ysidues: 1-360 KSTO>
toss-references: GB.AP001512; GB:BA000004; NID:g10174030; PIDN:BAB05174.1;
Experimental source: strain C-125
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                                                                                                                                                                                                                                                                                                                            94.1%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97.1%;
                                                                                                                                                                                                                                                                                                          Score 32; DB
Pred. No. 23;
1; Mismatches
                                                                                                                                                                                                                                                                                                            1:
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Pred.
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                                                                                                                                                                                                                                                                                                                          DB
23;
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                                                                                                                                                                                                                                                                                                                                             Length 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                              GSPDB: GN00140
                                                                                                                                                                                                                                                                                                          0;
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                                                       A; Gene: Cj1413
C; Superfamily:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: At2g18740
Query Match
Best Local Similarity
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                                                                             Cj1413c
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A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: A84568 A;Accession: A84568 A;Status: preliminary
                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-88 <STO>
                                                                                                                                                                                                                                                      A;Cross-references: GB:AE002093; NID:g4185140; PIDN:AAD08943.1;
                                                                             27 IQIWLF
                                                                                                                                         Local Similarity
les 5; Conserv
                                                                                                            1 IQIWIF
                                                                                32
                                                                                                             6
                                                                                                                                             Conservative
                                                                                                                                                          94.1%;
                                                                                                                                                          Score 32;
Pred. No.
                                                                                                                                             Mismatches
                                                                                                                                                        DB
23;
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                                                                                                                                                                        Length
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Sarcophyton glaucum mitochond
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                                                                                                                                         Gaps
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A; Note: ND4
C; Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C; Keywords: membrane-associated complex; mitochondrion; A; Molecule type: DNA A; Residues: 1-495 <BEA> R;Beaton, M.J.; Roger, A.J.; Cavalier-Smith, T.
J. Mol. Evol. 47, 697-708, 1998
A;Title: Sequence analysis of the mitochondrial genome (
A;Reference number: Z17505; MUID:99065763; PMID:9847412
A;Accession: T12401
A;Status: preliminary; translated from GB/EMBL/DDBJ NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - Sarcophyton glaucum C;Species: mitochondrion Sarcophyton glaucum C;Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 03-Jun-2002 C;Accession: T12401 A; Genome: mitochondrion A;Cross-references: EMBL:AF064823; NID:g4091912; PID:g4091917; of Sarcophyton PIDN:AAC99651 glaucum: Conser

Query Match Best Local Similarity 219 IQIWLF 224 1 IQIWIF 6 Conservative 94.1%; 83.3%; ۲, Score 32; | Pred. No. 1 Mismatches BB JB 2; ⊥.3e+02; 0; Length 495; Indels 0 0

NAD; oxidative phosphorylatio

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-394 <PAR> probable polysaccharide modification protein Cj1413c [imported] - Campyloba C;Species: Campylobacter jejuni C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 03-Jun-2002 A;Cross-references: GB:AL139078; GB:AL111168; NID:g6968723; PIDN:CAB73837.1; A;Experimental source: serotype O2, strain NCTC 11168 A; Title: The genome sequence A; Reference number: A81250; NA; Accession: E81286 C;Accession: E81286
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C. R;Parkhill, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Nature 403, 665-668, 2000 kpsD protein of the food-borne pathogen Campylobacter jejuni MUID:20150912; PMID:10688204 [imported] - Campylobacter jejun Whitehead, PID: 9696 reveals s:

91.2%;

Score Pred.

31; No.

DB 2; 1.6e+02;

Length

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Tibosomal protein S3, chloroplast - spinach chloroplast C;Species: chloroplast Spinacia oleracea (spinach) C;Date 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 22-Jun-1999 C;Accession: S01978 R;Zhou, D.X.; Quigley, F; Massenet, O.; Mache, R. Mol. Genet. 216, 439-445, 1989 A;Title: Cotranscription of the S10- and spc-like operons in spinach chloro A;Reference number: S01976; MUID:89313684; PMID:2747623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Reference number: A38013
A;Contents: annotation; gene organization, sites, features
R;Tanaka, M; Waksugi, T; Sugita, M; Shinozaki, K; Sugiura, M.
Proc. Natl. Acad. Sci. U.S.A. 83, 6030-6034, 1986
A;Title: Genes for the eight ribosomal proteins are clustered on the chloroplast genome
A;Reference number: A94118; MUID:86287388; PMID:3016736
A;Accession: E25943
A;Accession: E25943
A;Holecule type: DNA
A;Residues: 1-218 <TAN>
C;Genetics:
A;Genes: rps3
A;Genes: rp
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C;Superfamily: Escherichia coli ribosomal protein
C;Keywords: chloroplast; protein biosynthesis; rik
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                                                                                                                                                                                           C; Keywords: chloroplast;
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Shinozaki, K.; Ohme, M.; Tanaka, M.; Wakasugi, T.; Hayashida, N.; Watsubaya
eno, H.; Kanogashira, T.; Yamada, K.; Kusuda, J.; Takaiwa, F.; Kato, A.; Toh
EMBO J. 5, 2043-2049, 1986
EMBO J. 5, 2043-2049, 1986
EMBO J. 5, 2043-2049, 1986
                                                                                                                                                                                                                                                                      A; Genome:
                                                                                                                                                                                                                                                                                              A; Gene: rps3
                                                                                                                                                                                                                                                                                                                            C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-218 <ZHO>
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A; Residues: 1-218 <SUG>
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Best Local S
Matches 5
                                                                                                                                                                                                                                ;Genome: chloroplast;Superfamily: Escherichia coli ribosomal protein
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;Keywords: chloroplast;
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      IQIWIF 6
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                                                                Similarity 5; Conserv
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83.3%;
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                                                                                               Score 30;
Pred. No.
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Pred. No.
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0;
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Kato, A.; Tohdoh,
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ribosomal protein S3, mitochondrial - red alga (Chondrus crispus) mitochondrion c;Species: mitochondrion Chondrus crispus (carragheen) C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 21-Jul-2000 C;Accession: S59085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Reference number: A70300; MUID:98196666; PMID:9537320 A;Accession: E70340
R;Leblanc, C.; Boyen, C.; Richard, O.; Bonnard, G.; Grienenberger, J.M.; Kloareg, J. Mol. Biol. 250, 484-495, 1995
A;Title: Complete sequence of the mitochondrial DNA of the rhodophyte Chondrus cri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glutaredoxin-like protein - Aquifex aeolicus
C;Spectes: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C;Accession: E70340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ribosomal protein S3, plastid - beechdrops plastid
C;Species: plastid Epifagus virginiana (beechdrops)
C;Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 13-Aug-1999
C;Accession: S78395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Deckert,
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J. Mol. Evol. 35,
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| 138 | IEIWVF | 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1-229 <AQF>
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Pred. No. 1.4e+02;
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  mitochondrial DNA of the rhodophyte Chondrus crispu
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C:Genetics:
A:Gene: CESP:C02F12.1
A:Introns: 23/3; 58/3; 83/3; 140/3; 178/3; 257/3;
                                                                                                                                                                                                                                                             related to cell protein precursor [imported] - Neurospora crassa N;Alternate names: protein B24P7.180 C;Species: Neurospora crassa C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change C;Accession: T50963
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Best Local Similarity
Them 5; Conserve
                  C; Genetics:
A; Gene: NCSP: B24P7.180
                                                                                                                                                                                                                      R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; submitted to the Protein Sequence Database, July 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, November 1995 A;Description: The sequence of C. elegans cosmid C02F12. A;Reference number: Z21473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T34080
R;Miller, N.
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A;Accession: S59085
A;Status: nucleic acid sequence not shown; translation:
A;Molecule type: DNA
A;Residues: 1-240 <LEB>
A;Map
                                                              A; Experimental source: BAC
                                                                                     A; Cross-references:
                                                                                                          A; Molecule type: DNA
A; Residues: 1-347 <SCH>
                                                                                                                                                 A; Status: preliminary
                                                                                                                                                                          A; Reference number: Z25286
A; Accession: T50963
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein C02F12.1 - Caenorhabditis elegans
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A;Experimental source: strain NCTC 3438
C;Superfamily: Haemophilus paragallinarum type II site-specific deoxyribonuclease
                                                                                                                                                                                                                                                                              A;Status: preliminary; not compared with conceptual translation A;Molecule type: DNA A;Residues: 1-488 <SUG>
                                                                                                                                                                                                                                                                                                                               Bull Inst Chem Res Kyoto Univ. 71, 338-342, 1993
A;Title: Nucleotide sequence of the gene of HgaI restriction endonuclease.
A;Reference number: A59239
A;Accession: C59240
                                                                                                                                                                                                                                                                                                                                                                                                                     type II site-specific deoxyribonuclease (EC 3.1.21.4) HgaI - Haemophilus paragallinar
C;Species: Haemophilus paragallinarum
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 20-Jun-2000
C;Accession: C59240
Search completed: January Job time: 10.9545 secs
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
     of hits satisfying chosen parameters:
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00 80	Acinet Bacter	Acinetobacter calcoaceticus. Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae	ceae;
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RP RC	SEQUEN	SEQUENCE FROM N.A. STRAIN-BD413 / ADP1;	
RX RA	MEDLIN	r W., Frosch C.S., Haspel G., Ehrt S	en W.;
RT	"Two c	ing proteins with similarities to	oxi
Z P R	lauric Microb	auric acid in Acinetobacter calcoaceticus ADP1."; Ecrobiology 141:1425-1432(1995). 21	
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RX	MEDLIN	228433; PubMed=9074511;	
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388		PATHWAY: FINAL STAGES IN PEPTIDOGLYCAN SYNTHESIS	- 14
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Query Match
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Matches 5; Conservative

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Interpro; IPR004044; KH_TYPE_2.
Interpro; IPR001351; Ribosomal_S.
Pfam; PF00189; Ribosomal_S.C; 1.
Pfam; PF00417; Ribosomal_S.N; 1.
TICRFAMS; TIGR01009; rPSC_bact; 1.
PROSITE; PS00823; KH_TYPE_2; 1.
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Spinacia oleracea
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SIMILARITY: BELONGS TO THE S3P FAMILY OF RIBOSOMAL PROTEINS SIMILARITY: CONTAINS 1 KH TYPE-2 DOMAIN.
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InterPro; IPR001351; Ribosomal_S3.
Pfam; PF00189; Ribosomal_S3_C; 1.
Pfam; PF00417; Ribosomal_S3_N; 1.
TIGRPAMS; TIGR01009; TPSC_bact; 1.
PROSITE; PS50823; KH_TYPE_2; 1.
PROSITE; PS50823; KH_TYPE_3; 1.
PROSITE; PS00548; RIBOSOMAL_S3; 1.
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STRAIN-cv. Br.
Shinozaki K.,
                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
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the European Bioinformatics Institute
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"The plastid chromosome of spinach (Spinacia nucleotide sequence and gene organization.";
plant Mol. Biol. 45:307-315(2001).
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                                                                                                                                       NCBI_TaxID=4097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X13336; CAA31715.1;
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5; Conserv
                                   Bright Yellow 4;
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   Ohme M.,
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   Tanaka
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               agreement (See
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InterPro; IPR001351; Ribosomal_S3.
pfam; pF00189; Ribosomal_S3_C; 1.
pfam; pF00417; Ribosomal_S3_K; 1.
TIGREAMS; TIGR01009; TPSC_bact; 1.
pROSITE; PS50823; KH_TYPE_2; 1.
pROSITE; PS00548; RIBOSOMAL_S3; 1.
                                 [1]
SEQUENCE FROM N.A.
MEDLINE-93066301; PubMed=1332054;
Wolfe K.H., Morden C.W., Palmer J.D.;
Wolfe K.H., Morden C.W., Palmer J.D.;
Punction and evolution of a minimal plastid nonphotosynthetic parasitic plant.";

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P30055;
01-APR-1993
01-APR-1993
15-JUN-2002
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Tanaka M., Wakasugi T., Sugita M., Shinozaki K., Sugita M.;
Tanaka M., Wakasugi T., Sugita M., Shinozaki K., Sugita M.;
Tanaka M., Wakasugi T., Sugita M.;
Tanaka M., Sugita M.;
Tanaka M., Sugita M.;
Tanaka M., Sugita M.;
Tanaka M.;
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SEQUENCE FROM N.A. MEDLINE=93021155; PubMed=1404416;
                                                                                                                                                                                                                                                                   Spermatophyta; Magnol Asteridae; euasterids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                            NCBI_TaxID=4177;
                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                             Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                    Epifagus virginiana
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Yamaguchi-Shinozaki K., Ohto C., Torazawa K., Meng B.-Y., Sugita
Deno H., Kamogashira T., Yamada K., Kusuda J., Takaiwa F., Kato
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(Rel. 25, Last sequence update)
(Rel. 41, Last annotation update)
30S ribosomal protein S3.
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sterids I; Lamia
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83.3%;
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RESULT 6
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Best Local
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01-FEB-1996
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                                                                                            This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                        J. MOL. Biol. 250:484-495(1995).
-!- SUBCELLULAR LOCATION: Mitochondrial.
-!- SIMILARITY: BELONGS TO THE S3P FAMILY OF RIBOSOMAL PROTEINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a obetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Rapid evolution of the plastid translational nonphotosynthetic plant: loss or accelerated trNA and ribosomal protein genes.";

Mol. Evol. 35:304-317(1992).

-!- SIMILARITY: CONTAINS 1 KH TYPE-2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGRFAMS; TIGR01009; rpsC_bact; 1.
PROSITE; PS50823; KH_TYPE_2; FALSE_NEG
PROSITE; PS00548; RIBOSOMAL_S3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed.
                                     EMBL; Z47547; CAA87601.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              organization."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chondrus crispus (Gigartinales).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kloareg B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95341681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=2769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chondrus crispus (Carragheen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitochondrial ribosomal protein
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   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Apices
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ribosomal protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete sequence of the mitochondrial DNA of the rhodophyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leblanc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             211 IKIWIF 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C., Boyen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 33, Last sequence up
(Rel. 33, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=7616569;
C., Richard O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chloroplast
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83.3%;
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   Ribosomal_S3
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blastid translational
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; 5BF70AC74AB7DF94 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bonnard G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gigartinales; Gigartinaceae;
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                                                                                                                       http://www.isb-sib.ch/announce/
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RESULT 8
T2G1_HAEGA
ID T2G1_HAEGA
AC P43418;
DT 01-NOV-1995
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                                                                                                                                      Query Match
Best Local Similarity
Thes 5; Conserv
                                                                                                                                                                                                    SQ SQ
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YL11_CAEEL
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Best Local :
            01-NOV-1995 (Rel.
                                                                                                                                                                                                                      InterPro; IPRO00301; Transmem_4.

Pfam; PF00335; transmembrane4; 1.

PROSITE; PS00421; TM4_1; FALSE_NEG.

Hypothetical protein; Transmembrane.
TRANSMEM 29 49 POTENTI.
TRANSMEM 54 74 POTENTI.
                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q11098;

Q1-NOV-1997 (Rel. 35, Created)

15-JUN-2002 (Rel. 41, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

Hypothetical protein CO2F12.1 in chromosome x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam;
Pfam;
                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a chetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .....yura; metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C02F12.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00548; RIBOSOMAL_S3; FALSE_NEG Ribosomal protein; Mitochondrion. SEQUENCE 240 AA; 28142 MW; C910AA2E6D
                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted
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                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Waterston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (NOV-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Miller N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-Bristol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                  238 QIWIF 242
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                                                                                                                         2 QIWIF 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                    mitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
SUBCELLULAR LOCATION: Integral membrane protein (Potential).
SIMILARITY: SOME, TO THE TETRASPANIN (TM4SF) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF00189; Ribosomal_S3_C; 1. PF00417; Ribosomal_S3_N; 1.
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277 AA;
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                                     STANDARD;
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Pred. No.
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                                                                                                                                                                                                  8084221CBD4C541D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C910AA2E6D8C800E CRC64;
                                                                                                                                                 Mismatches
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RESULT 9
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use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                   Y052_BUCAI
P57160;
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                                                                                                                "Genome sequence of the Buchnera sp. APS.";
Nature 407:81-86(2000).
                                                                                                                                                         MEDLINE=20445173; PubMed=10993077;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
"Genome sequence of the endocellular bacterial symbiont of aphids
                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-Tokyo 1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D17388; BAA04208.1; -. REBASE; 1096; HqaI.
                                                                                                                                                                                                                                                   NCBI_TaxID=118099;
                                                                                                                                                                                                                                                            symbiotic bacterium).
Bacteria; Proteobacteria; gamma subdivision; Buchnera
                                                                                                                                                                                                                                                                                               Buchnera aphidicola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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specific double-stranded fragments with terminal 5'-phosphates.
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                                                                                                                                                                                                                                                                                                                          Hypothetical
                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Nucleotide sequence of the gene of HgaI restriction endonuclease.";
Bull. Inst. Chem. Res., Kyoto Univ. 71:338-342(1993).

-i- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCES GACGC AND GCG-
AND CLEAVES RESPECTIVELY 10 BASES AFTER G-1 AND 10 BASES BEFORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sugisaki H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-NCTC 3438;
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40, Last annotation updat
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100.0%;
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7 MW; B5E05259E3C710D2
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Pred. No.
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05259E3C710D2 CRC64;
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                                       ormatics and the EMBL outstation There are no restrictions on it ing as its content is in no wa
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               http://www.isb-sib.ch/announce,
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Matches 5
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O9MUU2;
16-OCT-2001 (Rel. 40, Createu,
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
^hloroplast 30S ribosomal protein S3.
                                                                                                                                                                         Pfam; PF00013; KH-domain; 1.
Pfam; PF00189; Ribosomal_S3_C; 1.
Pfam; PF00417; Ribosomal_S3_N; 1.
SMART; SM00322; KH; 1.
                                                                                                                                      TIGRFAMS; TIGR01009; rpsc_bact; 1.
PROSITE; PS50823; KH_TYPE_2; 1.
PROSITE; PS00548; RIBOSOMAL_S3; 1.
                                                                                                                                                                                                                            EMBL; AF166114; AAF43809.1; -.
InterPro; IPR004044; KH_TYPE_2.
InterPro; IPR004087; KH_dom.
InterPro; IPR001351; Ribosomal_S3.
                                                                                                                                                                                                                                                                                                                                                                                              Lemieux C., Otis C., Turmel M.;
"Ancestral chloroplast genome in Mesostigma viride revenench of green plant evolution.";
Nature 403:649-652(2000).
-!- SIMILARITY: BELONGS TO THE S3P FAMILY OF RIBOSOMAL
-!- SIMILARITY: CONTAINS 1 KH TYPE-2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chloroplast.

Eukaryota; Viridiplantae; Streptophyta; Mesostigmatophyceae; Mesostigmatales; Mesostigmataceae; Mesostigma.
                                                                                                             Ribosomal protein;
DOMAIN 39
                                                                                                                                                                                                                                                                                            entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20150907; Put
Lemieux C., Otis C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RR3_MESVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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200 IKVWIF 205
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5; Conserv
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4; Conser
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PS00548; RIBOSOMAL_S3; 1.
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                                                                                                                         Chloroplast.
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16921 MW; 87D669CDAD999ECB CRC64;
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66.7%;
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                                              Pred. No. 90;
2; Mismatches
                                                                      Score 29;
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61;
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RESULT 11
RR3_MARPO
ID RR3_M
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Best Local
RR3_MAIZE
P06586;
01-JAN-1988
01-JAN-1988
15-JUN-2002
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01-JAN-1988
15-JUN-2002
Chloroplast
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Umesono K., Shiki Y., Ta
Ozeki H.,
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P06356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001351; Ribosomal_S3.C; 1.
Pfam; PF00189; Ribosomal_S3_N; 1.
Pfam; PF00417; Ribosomal_S3_N; 1.
TIGRRAMS; TIGR01009; rpsC_bact; 1.
PROSITE; PS50823; KH_TYPE_2; 1.
PROSITE; PS00548; RIBOSOMAL_S3; 1.
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J. Mol. Biol. 203:333-351(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ribosomal protein;
DOMAIN 46
SEQUENCE 217 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license according to the statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              liverwort Marchantia polymorpha chloroplast DNA.";
Nature 322:572-574(1986).
-!- SIMILARITY: BELONGS TO THE S3P FAMILY OF RIBOSOMAL PROTEINS.
-!- SIMILARITY: CONTAINS 1 KH TYPE-2 DOMAIN.
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MEDLINE=89068687; PubMed=3199436;
Fukuzawa H., Kohchi T., Sano T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Marchantiopsida; Marchantii
Marchantiaceae; Marchantia.
MASI_TaxID=3197;
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InterPro; IPR001351; Ribosomal_
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                                                                                                                                                                                                                                                                                                                 208 IKVWIF 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 29;
Pred. No.
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Chang Z., A
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Inokuchi H.,
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15-JUL-1998 (Rel. 36, List s
15-JUN-2002 (Rel. 41, Last a
15-JUN-2002 (Rel. 41, Last a
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SEQUENCE FROM N.A.
STRAIN-IAM C-27 / 7
MEDLINE-97303241; 1
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Chlorella vulgaris.
                                                                                                                                                                                                                 Eukaryota; Viridiplantae;
Chlorellaceae; Chlorella.
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Pfam; PF00199; Ribosomal_S3_C; 1.
Pfam; PF00417; Ribosomal_S3_L; 1.
TIGRFAMS; TIGR01009; rpsC_bact; 1.
PROSITE; PS50823; KH_TYPE_2; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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J. Mol. Biol. 251:614-628(1995).
-I- SIMILARITY: BELONGS TO THE S3P FAMILY OF RIBOSOMAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95395841; FUDITED TOTAL TOTAL MAIET R.M., Neckermann K., Igloi G.L., Koessel H.;
Maier R.M., Neckermann K., Igloi G.L., Koessel H.;
"Complete sequence of the maize chloroplast genome: gene content,"
"Complete sequence and fine tuning of genetic information by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zea mays (Maize).

Chloroplast.
Chloroplast.
Chloroplast.
Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC cl
                                                                                                                                                                              NCBI_TaxID=3077;
                                                                                                                                                                                                                                                                                            Chloroplast
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                McLaughlin W.E., Larrinua I.M.; "The sequence of the maize plastid encoded rps3 locus."; Nucleic Acids Res. 15:4689-4689(1987).
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NCBI_TaxID=4577;
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                           Tamiya;
PubMed-9159184;
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Last annotation update)
omal protein S3.
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Pred. No. 95;
2; Mismatches
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RESULT 14
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InterPor; IPR004044; KH_TYPEE_2.
InterPor; IPR001351; Ribosomal_S3.
Pfam; PF00189; Ribosomal_S3_C; 1.
Pfam; PF00417; Ribosomal_S3_N; 1.
TIGNEAMS; TIGR01009; TPSC_bact; 1.
PROSITE; PS0823; KH_TYPE_2; 1.
PROSITE; PS00548; RIBOSOMAL_S3; 1.
                                                                                                                                                      Hiratsuka J., Shimada H., Whittier R., Ishibashi T., Sakamoto M., Mori M., Kondo C., Honji Y., Sun C.-R., Meng B.-Y., Li Y.-Q., Kanno A., Nishizawa Y., Hirai A., Shinozaki K., Sugiura M.; Kanno A., Rishizawa Y., Hirai A., Shinozaki K., Sugiura M.; "The complete sequence of the rice (Oryza sativa) chloroplast genome: intermolecular recombination between distinct tRNA genes accounts for a major plastid DNA inversion during the evolution of the cereals.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RR3_ORYSA
P12146;
                                                                                                   a major plastid DNA inversion during the evolution Mol. Gen. Genet. 217:185-194(1989).
-i- SIMILARITY: BELONGS TO THE S3P FAMILY OF RIBOSC-i- SIMILARITY: CONTAINS 1 KH TYPE-2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                             Spermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT 1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Chloroplast 30S ribosomal protein S3.
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"Complete nucleotide sequence of the chloroplast genome green alga Chlorella vulgaris: the existence of genes po involved in chloroplast division.";
Proc. Natl. Acad. Sci. U.S.A. 94:5967-5972(1997).
-i- SIMILARITY: BELONGS TO THE 33P FAMILY OF RIBOSOMAL P.-i- SIMILARITY: CONTAINS 1 KH TYPE-2 DOMAIN.
             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no we
                                                                                                                                                                                                                                                                      STRAIN=cv. Nipponbare; MEDLINE=89364698; PubMed=2770692;
                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (Rice).
Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                         STRAIN-CV.
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4530;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tsudzuki J.,
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-profit institutions a
this statement is not
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Nakashima K., Tsudzuki T., S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chloroplast.
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2; Mismatches
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Pred. No.
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Suzuki Y., Hamada
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                                                                                                                          RIBOSOMAL PROTEINS
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                                                    a collaboration -
MBL outstation -
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RESULT 15
RS3_SYNY3
   Query Match
Best Local Similarity
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                                                            InterPro; IPRO04044; KH_TYPE_2.
InterPro; IPRO04087; KH_dom.
InterPro; IPR004088; KH_type_1.
InterPro; IPR001351; Kibosomal_S3.
Pfam; PF00013; KH-domain; 1.
Pfam; PF00189; Ribosomal_S3_C; 1.
Pfam; PF00189; Ribosomal_S3_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RS3_SYNY3
P73314;
01-NOV-1997
01-NOV-1997
16-OCT-2001
                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                             Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yasuda M., Tabata S.; Yamada M., Yasuda M., Tabata S.; "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein coding regions."; DNA Res. 3:109-136(1996).

-i- FUNCTION: THIS PROTEIN IS INVOLVED IN THE BINDING OF INITIATOR MET-TRNA (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis
NCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro: IPR001351; Ribosomal_S3. Pfam; PF00189; Ribosomal_S3.C; 1. Pfam; PF00417; Ribosomal_S3.N; 1. TIGRFAMs; TIGR01009; rpsc_bact; 1. PROSITE; PS50823; KH_TYPE_2; FALSE_NEG. PROSITE; PS00548; RIBOSOMAL_S3; 1. Ribosomal protein; Chloroplast.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                 EMBL; D90905; BAA17343.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kaneko T., Sato S., Kotani H., Tanaka
Miyajima N., Hirosawa M., Sugiura M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30S ribosomal protein S3 RPSC OR RPS3 OR SLL1804.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; x15901; CAA33934.1; PIR; JQ0265; R3RZ3.
                               SMART; SM00322; KH; 1.
TIGRFAMS; TIGR01009; r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-97061201; PubMed-8905231;
Kaneko T., Sato S., Kotani_H., Tanaka A., Asamizu E., Nakamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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PS50823; KH_TYPE_2; 1.
PS00548; RIBOSOMAL_S3; 1.
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(Rel. 35, Last sequence update)
(Rel. 40, Last annotation update)
al protein S3.
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                                                Query Match
Best Local 9
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                                                                                    Ribosomal protein; trNA-binding; Complete proteome INIT_MET 0 0 BY SIMILARITY.

DOMAIN 64 100 KH TYPE-2
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199 IKVWIF 204
                   1 IQIWIF 6
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239 /
                                      Conservative
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27016 MW;
                                                85.3%;
                                    Score 29; DB Pred. No. 1e+0 2; Mismatches
                                                                             0664CE072B38C6B2 CRC64;
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Search completed: January Job time: 6.18182 secs

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Result
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Maximum DB seq length: 2000000000
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Sp_archea:*

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sp_beteria

sp_fungi:*

sp_human:*

sp_mamma

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                                                                                                                                                                                                                                                                                                                                                   Score
        Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           January 3, 2003, 15:24:35; Search time 20,3182 Seconds (without alignments) 60.846 Million cell updates/sec
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Gapop 10.0 ,
      671580 seqs, 206047115 residues
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sp_rvirus:*
sp_bacteriap:*
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sp_virus:*
sp_vertebrate:*
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sp_bacteria:*
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Compugen Ltd.
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Q9zzn7 cyanidiosch
Q17997 caenorhabdi
Q9kcw4 bacillus ha
Q9mcc7 arabidopsis
Q9zv45 arabidopsis
Q9zv45 arabidopsis
Q9zv45 arabidopsis
Q9zv45 arabidopsis
Q9zv46 arabidopsis
Q9zv47 arabidopsis
Q9zv47 arabidopsis
Q9zv47 arabidopsis
Q9mp4 campylobact
Q8mp14 desulfitoba
Q9mp4 campylobact
Q8mp14 desulfitoba
Q9cu03 mus musculu
Q9mt17 oenothera h
Q8s8v5 atropa bell
Q68753 aquifex aeo
Q9p3r7 neurospora
Q9rnel bacillus an
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080809	Q9SPE8	Q9SPE9	Q8WR60	Q9HIF5	064861	Q9G8Q4	Q9C473	061643	051706	P74743	Q9CZV2	Q8VQR8	099992	Q8UE24	Q95H49	Q9CL37	Q97P66	Q9TL20	Q8RIG1	Q9BBP8	098455	Q8R460	061555	Q8W0K1	Q97C83	Q9HLS6	085468	Q973N4
	۳.	Q9spe9 arabidopsis			O64861 arabidopsis	aegleria	Q9c473 emericella	Q.	O51706 borrelia bu	P74743 synechocyst	Q9czv2 mus musculu	hytoplas	099992 porphyra pu	Q8ue24 agrobacteri	Q95h49 triticum ae		Q97p66 streptococc	Q9tl20 nephroselmi	Q8rig1 fusobacteri	Q9bbp8 lotus japon	ij	Q8r460 mus musculu	drosoph	Q8w0k1 oryza sativ	Q97c83 thermoplasm	Q9hls6 thermoplasm	5468 ba	Q973n4 sulfolobus

# ALIGNMENTS

RE	RESULT 1	
29	Q9zzn7	
ID		
AC	Q9ZZN7;	
DΤ	01-MAY-1999 (TrEMBLrel.	
DT	01-MAY-1999 (TrEMBLrel. 10,	
DT	01-MAR-2002 (TrEMBLrel. 20,	
DE	30S ribosomal protein S3.	
GN		
SO		
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ox Ox	NCBI_TaxID=45157;	
RN		
RP		
RC	STRAIN=10D;	
RX	MEDLINE-99030526; PubMed-9801318;	
RA		
RT		
RT	unicellular red alga Cyanidioschyzon merolae deduced from the complete	
RT	nucleotide sequence.";	
RL		
DR		
DR		
DR	Pfam; PF00189; Ribosomal_S3_C; 1.	
KW	Mitochondrion; Ribosomal protein.	
QS	SEQUENCE 282 AA; 33871 MW; 89CC910DAA22DFB2 CRC64;	
	Query Match 97.1%; Score 33; DB 8; Length 282; Best Local Similarity 83.3%; Pred. No. 1e+02; Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
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Z Z	RESULT 2	

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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spore BH1455
                                                                                                                                                           SEQUENCE
                                                                                                                                                                                             "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).
                                                                                                                                                                                                                                                                                                                 STRAIN-C-125 / JCM 9153;
MEDLINE-20512582; PubMed-11058132;
Takami H., Nakasone K., Takaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillaceae; Bacillus
NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09KCW4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z81109; CAB03254.1;
InterPro; IPR003003; 7TM_Chemo2.
InterPro; IPR000168; 7TM_nematode.
Pfam; PF01604; 7tm_5; 1.
                                                                                                                                                                            Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus halodurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
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R10D12.11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                Horikoshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        investigating
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109
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                                     IQIWIF 6
IQIWVF
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                                                                            Similarity
5; Conserv
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5; Conserv
                                                                                                                                                                                                                                                                                                   Hirama C., Nakamura Y.,
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0 (TrembLrel. 15,
0 (TrembLrel. 15,
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                                                                            Conservative
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                                                                                                                                                         41587 MW;
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                                                                                             97.1%;
83.3%;
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Last sequence update)
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Last sequence up
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Pred. No.
                                                                                               Pred. No. 1.3e+02;
                                                                                                                  Score 33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                              Y., Maeno G., Sa., Ogasawara N.,
                                                                                                                                                       1B25DCA9D4F6E328 CRC64;
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                                                                                                                  DB 16;
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                                                                                                                                                                                                                                                                                            Sasaki R., M
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                                                                                                                Length 360;
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RESULT 4

Q9MOCT
ID Q9MO
AC Q9MO
AC Q9MO
DT 01-0
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GN AT46
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RN [2]
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   DAC OCCUPANT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δÃ
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Matches 5
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01-MAY-1999 (TrEMBLrel. 10, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
Putative small nuclear ribonucleoprotein E.
AT2018740.
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Q9ZV45;
Q1-MAY-1999
Q1-MAY-1999
Q1-DEC-2001
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Q9M0C7;
Q1-OCT-2000
Q1-OCT-2000
Q1-JUN-2001
                                                                                                                                                                                                                                                                                                                                            STRAIN-CV. COLUMBIA;
MEDLIKE=20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eddicotyledons; core et
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ
EMBL; AL161576; CABB1026.1; -
Interpro; IPR001163; SNRNP_SM.
PF4m; PF01423; Sm; 1.
                                Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AC005724; AD08943.1; -.
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Mayer K.F.X.;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheopspermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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                                                                                                                                       STRAIN=CV.
                                                                                                                                                                                                                                                                              "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.";
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                                                                                                         Lin X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=3702;
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                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                 Nature
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es 5; Conserv
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                                                                                                                                   ROM N.A.
COLUMBIA;
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snRNP_Sm
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Last annotation updat
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No.
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Best Local :
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Q9CLF4;
Q1-JUN-2001
01-JUN-2001
01-JUN-2002
                                                                                                                                                                                       063853;
01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1999 (TrEMBLrel. 11, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01423; Sm; 1.
Nucleocapsid; Ribonuc
SEQUENCE 88 AA; 10
                                         Beaton M.J., Roger A.J., Cavalier-Smith T.;
"Sequence analysis of the mitochondrial genome of Sarcophyton glaucum: conserved gene order among octocorals.";
J. Mol. Evol. 47:697-708(1998).
                                                                                                                                                                                 NADH
  MEDLINE-98210232;
Pont-Kingdon G.,
                        SEQUENCE OF
                                                                                SEQUENCE FROM N.A.
MEDLINE=99065763; PubMed=9847412;
                                                                                                                           Eukaryota; Metazoa; Cnida Alcyoniidae; Sarcophyton.
                                                                                                                                                 Mitochondrion.
                                                                                                                                                           Sarcophyton glaucum
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                                                                                                                                                                                                                                                                                                                                                                                                              May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., K "Complete genomic sequence of Pasteurella multocida Pm70."; Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-PM70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical PM1281.
                                                                                                                  NCBI_TaxID=70919;
                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical
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5; Conserv
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291 AA; 3
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450-495 FROM N.A.
10232; PubMed-9541536;
n G., Okada N.A., Macf
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                                                                                                                                      Cnidaria;
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17, Last sequence update)
21, Last annotation update)
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l; Mismatches
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  Macfarlane
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                                                                                                                                      Anthozoa;
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52;
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 J.L.,
                                                                                                                                      Alcyonaria;
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1.7e+02;
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  Beagley C.T.,
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                                                                                                                                      Alcyonacea;
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RESULT 9
Q9PMP4
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Q93HD9
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Best Local Similarity
Thes 5; Conserva
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Wolstenholme D.R.;
Wiltochondrial DNA of the coral Sarcophyton glaucum contains a gene
Yelf for a homologue of bacterial MutS: a possible case of gene transfer
Yelf from the nucleus to the mitochondrion.";
Yelf J. Mol. Evol. 46:419-431(1998).
C. -!- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
YEMBL; AF064823; AAC99651.1; -.
YEMBL; AF064823; AAC99651.1; -.
YEMBL; AF063192; AAC16387.1; -.
YEMBL; AF063192
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Best Local Similarity
Matches 4; Conser
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O93HD9;
01-DEC-2001 (TremBLrel. 1
01-DEC-2001 (TremBLrel. 1
01-MAR-2002 (TremBLrel. 1
                                                                                                    01-OCT-2000
01-OCT-2000
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(200 EMBL; AB070945; BAB69249.1; -
Interpro; IPR000515; Babertansp.
Pfam; PF00528; BPD_transp; 1.
PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; UNKNOWN_PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; UNKNOWN_SEQUENCE 320 AA; 34176 MW; DD3BC5AB26756426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi (Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osono Kikuchi H., Shiba T., Sakaki Y., Hattori M.; "Genome sequence of an industrial microorganism Streptom avermitilis: Deducing the ability of producing secondary
                     Campylobacter jejuni.
Bacteria; Proteobacte
                                                             Possible polysaccharide CJ1413C.
Campylobacter
                                                                                                                                                                    Q9PMP4;
                                                                                                                                                                                        Q9PMP4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 metabolites."
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Bacteria; Firmicutes; Actinobacteria;
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                     Proteobacteria;
                                                                                                  (TrEMBLrel.) (TrEMBLrel.
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                                                                                                                                                                                          PRELIMINARY;
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66.7%;
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83.3%;
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19,
20,
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modification protein.
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Pred. No. 2.8e
2; Mismatches
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Pred. No. 2.8e+02;
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                   subdivision;
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Actinobacteridae;
Streptomyces.
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                 Campylobacter group;
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Matches
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SEQUENCE FROM N.A
                                                                              O9CUO3 PRELIMINARY; PRT; 115 AA.
O9CUO3;
O1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
1700116B05R1k protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                     Davis J.K., Tiedje J.M.;
"Sequence and transcriptional analysis of reductive dehalogenase of Desulfitobacterium.";
                               Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OBRPJ4 PRELIMINARY; PRT; 719 AA.
OBRPJ4;
O1-JUN-2002 (TrEMBLrel. 21, Created)
O1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 80.1 kDa protein.
                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                              Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases EMBL; AF403182; AAL87758.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-DCB-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia; Clostridiales; Peptococcaceae; Desulfitobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Desulfitobacterium hafniense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AL139078; CAB73837.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                reveals hypervariable sequences."; Nature 403:665-668(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20150912; PubMed=10688204;
Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd:
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitchead S., Barrell B.G.;
"The genome sequence of the food borne pathogen Campylobacter J."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-NCTC 11168; MEDLINE-20150912;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=49338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=197;
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                                                                                                                                                                                                                                 108 LQIWVF 113
                                                                                                                                                                                                                                                                                                                                                                                                                                           EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                     /pothetical protein.
EQUENCE 719 AA; 8
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                                                                                                                                                                                                                                                                                   Conservative
                                              Chordata;
Rodentia;
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                                                                                                                                                                                                                                                                                              91.2%;
66.7%;
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83.3%;
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Pred. No. 3.4e-
1; Mismatches
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                                                                                                                                                                                                                                                                                              Score 31; DB 2;
Pred. No. 6.2e+02;
                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                     B806F0F0F0F1D79B CRC64;
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                                                                                                                                                                                                                                                                                   Mismatches
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3.4e+02;
0;
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                                                                                                                                                                                                                                                                                                            Length 719;
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RESULT 12
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Best Local S
Matches 5
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Airawa K., Izawa M., Nishi K., Kiyoswa H., Kondo S., Yamanaka I.,
Ra Airawa K., Izawa M., Nishi K., Kiyoswa H., Kondo S., Yamanaka I.,
Ra Kadota K., Watsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schrimstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Myrons P., Marchionni L., Mashina J., Mazzarelli J., Mombaerts P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Sato K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 Query Match
Best Local Similarity
                                                                                  InterPro; IPR004044; KH_TYPE_2.
InterPro; IPR001351; Ribosomal_S3.C; 1.
Pfam; PF00189; Ribosomal_S3.C; 1.
Pfam; PF00417; Ribosomal_S3.N; 1.
TIGREAMS; TIGR01009; rPSC_bact; 1.
PROSITE; PS50823; KH_TYPE_2; 1.
PROSITE; PS00548; RIBOSOMAL_S3; UNKN
                                                Chloroplast.
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01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                         chromosome, representing plastome Eucenothera plastomes.";
                                                                                                                                                                                                                                                                                           Chiu W.L.,
                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids II; Myrtales; Onagraceae; Oenothera.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9MTI7
                                                                                                                                                                                                         Mol. Gen. Genet. 263:581-585(2000).
EMBL; AJ271079; CAB67198.1; -.
                                                                                                                                                                                                                                                                                                                               MEDLINE=20309318; PubMed=10852478;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oenothera hookeri (Hooker's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ribosomal protein
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EMBL; AK018963; BAB31497.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C57BL/6J; TISSUE=TESTIS; MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                            Hupfer H., Swiatek
                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=85636;
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                                                                                                                                                                                                                                                           Complete nucleotide sequence of the Oenothera elata plastid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 IRIWIF 45
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                                                     AA;
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                                                     24971 MW;
 88.2%;
83.3%;
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83.3%;
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15,
21,
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 Score
Pred.
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Pred. No.
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                                                     B0B741F658B010BA CRC64;
                                                                                                                                                                                                                                                                                                             S., Herrmann R.G., Maier R.M.,
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                                                                                     UNKNOWN_1.
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30;
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   DB 8;
3e+02;
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                 Length 218;
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RESULT 14
066753
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Best Local S
Matches 5
  Query Match
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066753; PRELIMINARY;

066753; O1-AUG-1998 (TYEMBLEL 07,

01-AUG-1998 (TYEMBLEL 07,

01-MAR-2002 (TYEMBLEL 20,
                                                 Complete SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The nucleotide sequence of the plastid chromosome of Atropa beliadonna (deadly nightshade) and its comparison with that a Nicotiana tabacum with emphasis on sequence elements relevant microevolution.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ316582; CAC88082.1;
                                                                                                                                                                                                                                       Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
"The complete genome of the hyperthermophilic bacterium Aquifex apolicus".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, Ribosomal protein S3.
                                                                                           InterPro; IPR000531; TonB_boxC.
PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
                                                                                                                       Nature 392:353-388(1998).

EMBL; AE000690; AAC06709.1; -.

InterPro; IPR000053; Thiored.

InterPro; IPR000531; TonB_boxC.
                                                                                                                                                                                                                             aeolicus
                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98196666; PubMed=9537320;
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aquifex aeolicus
Bacteria; Aquific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GUA OR AQ_443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glutaredoxin-like protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-AB5P(KAN);
Schmitz-Linneweber C.,
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; endicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Atropa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8S8V5;
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5; Conserv
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                                                    proteome.
229 AA;
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                                                    AA;
                                                    25640 MW;
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83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Solanales; Solanaceae; Atropa.
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Last annotation update)
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Pred. No.
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Submitted
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01-DEC-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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Schulte U., Aign V.,
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
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US-08-968-563-11
; Sequence 11, Application US/08968563
; Patent No. 6013494
; GENERAL INFORMATION:
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US-08-969-683A-11
, Sequence 11, Application US/08969683A
; Patent No. 6136576
; GENERAL INFORMATION:
APPLICANT: GENERCOR INTERNATIONAL, INC.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,601
APPLICATION NUMBER: 13, 1996
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
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ORIGINAL SOURCE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
TELEPHAX: 302-773-0164
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MEDIUM TYPE: 3.50 TOMPOTTEL
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,563
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CORRESPONDENCE ADDRESS:
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ANTHONY A. GATENBY
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                                                                                                                                                                                                                                                                                                                      unknown
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                                                                                                                                                                                               50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATENBY
                                                                                                                                                                                 Score 29; DB
Pred. No. 8.2e
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INC.
                                                                                                                                                                                               DB 3;
8.2e+02;
                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                             Length 391;
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US-09-297-928-7; Sequence 7, Application US/09297928; Patent No. 6358716; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/208
FILING DATE: 13 NOV-1997
APPLICATION NUMBER: 60/030,601
FILING DATE: 13 NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Glister, Debra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-864-7620
TELEFAX: 650-845-6504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/969,683A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: ME
TITLE OF INVENTION: PR
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Genencor International, Inc.
STREET: 4 Cambridge place
STREET: 1870 South Winton road
CITY: Rochester
                                                                                                                                                                                                                                                                                                                                                                                       68 VQMWVF 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity nes 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 33, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U
ZIP: 14618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                        1 IQIWIF 6
                           CORRESPONDENCE ADDRESS:
ADDRESSEE: GENENCOR INTERNATIONAL,
STREET: 4 CAMBRIDGE PLACE
1870 SOUTH WINTON ROAD
                                                                                                                                 LAREAU, RICHARD D.
TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF
GLYCEROL BY RECOMBINANT
                                                                                                                                                                                                                                           APPLICANT: BULTHUIS, BEN A.
                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                CITY: ROCHESTER
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ΝY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 391 amino acids
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                                                                                                                                                                                          HSU, AMY K.
                                                                                                                                                                                                          GATENBY, ANTHONY HAYNIE, SHARON L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
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                                                                                                                                                                                                                            ANTHONY A.
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                                                                                                                      ORGANISMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 29; DB 4; Le
Pred. No. 8.2e+02;
3; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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COMPUTER READABLE FORM: MEDIUM TYPE: DISKETTE, 3.5 INCH

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SEQUENCE DESCRIPTION: SEQ ID NO: 7: US-09-297-928-7
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US-08-919-624-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/919,624
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: NEW HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity hes 3; Conserv
                                                                                                                                                                                                                                           ZIP:
                                                                                                                                                                                                                                                                            CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 VOMWVF 73
                                                                                                                                                                                                                                                           COUNTRY:
                                                      APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CR-9981-P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/03602
FILING DATE: NOVEMBER 13, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                          94304
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Billings, Lucy J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 302-773-0164
TELEX: 6717325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: MICROSOFT WORD VERSION 7.0A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: MICROSOFT WINDOWS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lal, Preeti
Shah, Purvi
                                                                                                                                                                                                                                                           USA
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                                                                                                                                                                                                     Diskette
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50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 29; DB 4;
Pred. No. 8.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 391;
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; Sequence 18, Application US/09025151
; Patent No. 6187535
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                                                                                                                                                                                                                                             RESULT 7
US-09-065-474-145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Saccharomyces cerevisiae US-09-025-151-18
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                                                               Sequence 145, Application US/09065474
Patent NO. 6063599
GENERAL INFORMATION:
APPLICANT: Tang, Liang
APPLICANT: Blehm, E. Scot
TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: DEST THEREOF
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 18
LENGTH: 68
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                          Best
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APPLICANT: Fromont, Micheline
APPLICANT: Fromont, Micheline
APPLICANT: Fromont, Micheline
APPLICANT: Fromont, Micheline
APPLICANT: Rain, Jean-Chlistophe
TITLE OF INVENTION: FAST AND EXHAUSTIVE METHOD FOR SELECTING A PREY
TITLE OF INVENTION: INTEREST: APPLICATION TO THE CONSTRUCTION OF MAPS OF
TITLE OF INVENTION: INTERACTORS POLYPEPTIDES
FILE REFERENCE: 03495-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/025,151
CURRENT FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-845-4166 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: line
IMMEDIATE SOURCE:
LIBRARY: CARDN
CLONE: 282414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS: LENGTH: 433 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity tes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 415 CT. TO NO:
ADDRESSEE: Carol Talkington Verser,
ADDRESSEE: Heska Corporation
STREET: 1825 Share Point Drive
CITY: Fort Collins
                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity tes 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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50.0%;
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Pred. No.
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Pred. No. 8.9e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                         Length 68;
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COUNTRY:

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RESULT 8
US-09-557-034-145
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; MOLECULE TYPE:
US-09-065-474-145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 145, Application US/09557034
Patent No. 6365569
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO: 145:
SEQUENCE CHARACTERISTICS:
LENCTH: 287 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-5-(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 LRIWIF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 24-AP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Tang, Liang
APPLICANT: Tang, E. Scot
Blehm, E. Scot
TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN
PROTEINS, NUCLEIC ACID MOLECULES,
                                   ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-5-C1
                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: Windows 95 SOFTWARE: WordPerfect for Windows, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
TELECOMMUNICATION INFORMATION: TELEPHONE: 970/493-7272
                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
                                                                                                                                                                         APPLICATION NUMBER: US/09/557,034
FILING DATE: 21-Apr-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1825 Sharp Point Drive CITY: Fort Collins STATE: Colorado
                                                                                                                   APPLICATION NUMBER: 09/065,474 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Carol Talkington Verser, Ph.D. Heska Corporation
                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                              80525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-APR-1998
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Pred. No. 8.9e+02
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                                                                                                                                                                                                                                                           Version 7.0
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1 IQIWIF 6

159 LRIWIF 164

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; MOLECULE TYPE: US-09-031-485-2
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US-09-031-485-2
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   Query Match
Best Local S
Matches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09031485 Patent No. 5824306
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APPLICANT: Tang, Liang
APPLICANT: Blehm, E. Scot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                          PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/847,42

FILING DATE: 24 APPL1997

ATTORNEY/AGENT INFORMATION:

NAME: Verser, Carol Talkington

REGISTRATION UNUMBER: 37,459

REFERENCE/DOCKET NUMBER: HW-5
                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: DIR
TITLE OF INVENTION: PRO
TITLE OF INVENTION: USE
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 145: SEQUENCE CHARACTERISTICS: LENGTH: 287 amino acids
                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOTTWARE: WordPerfect for Windows,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
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nes 4; Conserv
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                  Local Similarity
                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Heska Corporation
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                                                                                                                            LENGTH:
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                                                                                                            amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
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    Conservative
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                                                                                                linear
                                                                                protein
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                  82.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82.4%;
                                                                                                                                                                                                                                                                                                         US/08/847,429
                                                                                                                                                                                                                                                                                                                                                                     US/09/031,485
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 Score 28; DB Pred. No. 9.6e 2; Mismatches
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Pred. No. 8
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9.6e+02;
0;
                                                                                                                                                                                                                                                                                                                                                                                                   Version 7.0
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                                  Length 312;
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US-08-847-429A-2

Sequence 2, Applic Patent No. 5827692

Application US/08847429A

Floppy disk

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TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 312 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-847-429A-2
                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
US-09-065-474-2
                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09065474 Patent No. 6063599
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Tang, Liang
APPLICANT: Blehm, E. Scot
                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                            APPLICANT: Tang, Liang
APPLICANT: Blebm, E. Scot
TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES, AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37, 459
REFERENCE/DOCKET NUMBER: HW-5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES, TITLE OF INVENTION: USES THEREOF
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  159 LRIWIF 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/847,429A FILING DATE: 24-APR-1997 CLASSIFICATION: 435
                                     COUNTRY:
                                                             CITY: Fort Collins
STATE: Colorado
                                                                                                  ADDRESSEE: Carol Talkington Verser, Ph.D ADDRESSEE: Heska Corporation STREET: 1825 Sharp Point Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                     80525
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66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 28; DB 2;
Pred. No. 9.6e+02;
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RESULT 12
US-09-557-034-2
; Sequence 2, Application US/09557034
; Patent No. 6365569
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local 9
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INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 312 amino acid
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NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/065,474
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TELECOMMUNICATION INFORMATION:
                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/557,034
FILING DATE: 21-Apr-2000
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION: <UNKnown>
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 09/065,474
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION UNMBER: 37,459
REPERENCE/DOCKET NUMBER: HW-5-C1
TELEPHONE: 970/493-7272
TELEPHONE: 970/493-7272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
COMPUTER: II
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tes 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 IQIWIF 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Tang, Liang
APPLICANT: Tang, Liang
Blebm, E. Scot
TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN
PROTEINS, NUCLEIC ACID MOLECULES, AND
                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 80525
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 17 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Carol Talkington Verser, Ph.D.
Heska Corporation
STREET: 1825 Sharp Point Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Fort Collins
                                      TELEFAX: 970/484-9505
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Colorado
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66.7%;
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Pred. No. 9.6e+02;
2; Mismatches 0;
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HOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-557-034-2
                              Query Match
Best Local Similarity
"hes 3; Conserve
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; SEO ID NO 5503
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5503
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                                                                                                                       ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-3703
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US-09-134-001C-5503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-09-134-001C-3703
                                                                                                                                                                                APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064, 964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5503, Apparent No. 63803
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Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RENERAL INFORMATION:

PPLICANT: Lynn Doucette-Stamm et al

ITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR APPLICATION NUMBER: US 60/0655,779

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-08-14
                                                                                                                                                             LENGTH: 496
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                 ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                quence 3703, Application US/09134001C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110 QIWLF 114
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   . 1 IQIWIF 6
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50.0%;
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                                             Mismatches
                                                                Score 28; DB 4;
Pred. No. 1.5e+03;
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Pred. No. 1.2e+03;
1; Mismatches (
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Pred. No. 9.6e+02
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Query Match
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Search completed: January Job time: 10 secs
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US-09-134-001C-3275
                                                                                                                                                                                                                                   APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NO 3275
LENGTH: 591
TYPE: PRT
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                                                                       359 VNIWIF 364
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                                                                                                                                             Conservative
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66.7%;
                    3, 2003, 15:34:30
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Pred. No. 1.7e+03;
1; Mismatches 1
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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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DB
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     Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

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9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

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13: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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   GenCore version Copyright (c) 1993 - 2003
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 9 US-09-736-457-31

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10 US-09-815-242-5172

10 US-09-815-242-1386

10 US-09-815-242-13969

10 US-09-815-242-11396

10 US-09-815-242-11103

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US-09-789-561-169
US-09-864-761-47624
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Compugen Ltd
Sequence 331, App
Sequence 331, App
Sequence 331, App
Sequence 1136, App
Sequence 5172, Ap
Sequence 316, App
Sequence 11369, A
Sequence 11592, A
Sequence 11592, A
Sequence 3652, Ap
Sequence 1254, App
Sequence 1254, App
Sequence 1254, App
Sequence 1269, Ap
Sequence 1269, Ap
Sequence 1269, Ap
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Sequence
Sequence
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169, App
47624, A
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Db Qy	Query M Best Lo Matches	0-SI	; SEQ 1D NO ; LENGTH: ; TYPE: P; ; ORGANIS;	1	; PRIOR ; PRIOR ; PRIOR ; PRIOR			RESULT 1 US-09-789-5 ; Sequence ; Patent NC ; GENERAL I		43 44 45	40 41 42	38 38	35 36	3 3 3 3 2 1	27 28 30	25 25 26	20 21 22
1 IQIWIF        86 INIWIF	Match Local Simi es 5;	NAME/KEY: SI LOCATION: (1 OTHER INFORM 9-789-561-92	. M:	PLI F S		LNE	H H	1 789-561-92 lence 92, A ent No. US2		2222	0 2 2 2 5 5 5 5	N N N の の の	2 2 2 5 6 6 6	27 27 26	27 27 27	27 27 27 27	27 27 27
91	ilarity Conserva	TE 43) ATION:	9 Homo sapiens	p SS R	N. N.	APPLICATION NUMBER FILING DATE: 2001	et al	pplicati 00200648 ATION:		76.5 76.5 76.5	200	ი ი ი		6.00	79.4 79.4 79.4	79.4 79.4 79.4 79.4	79.4 79.4
	85.3 83.3 ative	Xaa equ	ns	NUMBER: 1999-09 OS: 194 n Ver. 2.	JMBER: 2000-08 JMBER: 1999-09	UMBER: 2001-	52 Human	ion US, 318A1		337	253 253	242 245 245	111 139 197	805 93	572 573 573 608	384 411 466	110 264 283
	de de	equals		0-0	PCT/ 08-31 60/1 09-03	. US	nan	7097		9 10 10	999	တ ထ ထ	10 8 10	10 10	10010	10	10
	Score 29; DB 10; Length Pred. No. 1.7e+02; 0; Mismatches 1; Inde	any of the naturally		/152,315 3	F/US00/24008 7152,317 3	709/7 22	secreted proteins	709789561	ALIGNMENTS	US-09-815-242-11887	US-09-970-989-9 US-09-895-913A-130 US-09-860-670-115	US-08-818-581B-9 US-08-818-581B-13 US-09-970-989-4	-09-925-299 08-818-581B -09-811-284	US-09-815-242-5597 US-09-815-242-12286 US-09-864-761-45734	US-09-815-242-5626 US-09-815-242-12247 US-09-815-242-12921 US-09-924-358-8	US-09-738-626-6166 US-09-901-252-16 US-09-804-551B-14	S-09-867-550-298 S-09-925-301-905 -09-970-989-2
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	0;	ids								li pli pli	op Op	11	App App App	AP A	AP , A , A pli	Ap Appl Appl	App App App

RESULT 2 US-09-789-561-169 ; Sequence 169, Application US/09789561 ; Patent No. USZ0020064818A1 ; GENERAL INFORMATION:

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                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/207, 456
PRIOR FILING DATE: 2000-05-26
PRIOR PPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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SOFTWARE: Pac
SEQ ID NO 169
FRAGTH: 261
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LOCATION: (225)
OTHER INFORMATION: >
09-789-561-169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hanzel, David I APPLICANT: Chen, Wensheng
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CURRENT FILING DATE: 2001-05-23
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PRIOR FILING DATE: 1999-09-03
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PRIOR FILING DATE: 1999-09-03
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CURRENT FILING DATE: 2001-02-22
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APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
                                                                                   APPLICATION NUMBER: PCT/US01/00665
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
                                                                                                                                                                           APPLICATION NUMBER: PCT/US01/00669 FILING DATE: 2001-01-30
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Pred. No. 2.4e+02;
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PRIOR APPLICATION NUMBER: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2000-09-21
PRIOR PELING DATE: 2000-09-21
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/704, 203
PRIOR APPLICATION NUMBER: US 09/774, 203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEO ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine v
                                                                                                                                                             NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 331
LENGTH: 92
TYPE: PRT
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Best Local :
                                                               Matches
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                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/736,457 CURRENT FILING DATE: 2000-12-13
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                              APPLICANT: Wang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C15
                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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OTHER
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                                                                                                                                             ORGANISM: Homo sapiens
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                              1 IQIWIF 6
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IQVWLY 36
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3; Conservative
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Lodes, Michael
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Mannion, Jane
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                                                               Conservative
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NN: EXPRESSED IN HBLLOO, SIGNAL = 2.5
NN: EXPRESSED IN FELA, SIGNAL = 2.2
NN: EXPRESSED IN PLACENTA, SIGNAL = 1.1
NN: EXPRESSED IN BT474, SIGNAL = 2.3
NN: EXPRESSED IN BT474, SIGNAL = 2.3
NN: EXPRESSED IN BT474, SIGNAL = 1.1
NN: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
NN: SWISSPROT HIT: P08578, EVALUE 2.00e-16
NN: SWISSPROT HIT: BF680487.1, EVALUE 6.00e-31
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Michael A.
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Pred. No.
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Pred. No. 1.
                                                               Mismatches
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                                                        1.3e+02;
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US-09-902-941-331

GENERAL INFORMATION:

APPLICANT: Henderson, Robert A.

Patent No.

331, Application US/09902941 5. US20020172952A1

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DЬ
                                               Query Match
Best Local Similarity
"~+~hes 3; Conserve
                                                                                                                            : SEQ ID NO 331
LENGTH: 92
: TYPE: PRT
ORGANISM: Homo sapiens
US-09-849-626-331
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SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 331
LENGTH: 92
TYPE: PRT
ORGANISM: Homo sapiens
US-09-902-941-331
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Best Local S
Matches 3
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                                                                                                                                                                                                                                                                     APPLICANT: Wang, Aijun
APPLICANT: Wang, Tongtong
APPLICANT: Switzer, Anne
APPLICANT: Switzer, Anne
APPLICANT: Clapper, Jonathan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
EILE REFERENCE: 210121.478C16
                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/849,626
CURRENT FILING DATE: 2001-05-03
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SOFTWARE: FastSEQ for Windows Version 3.0
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URRENT APPLICATION NUMBER: US/09/902,941
URRENT FILING DATE: 2001-07-10
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31
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nes 3; Conserv
                               1 IQIWIF 6
IQVWLY 36
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Johnson, Jeffrey C.
                                                                                                                                                                                                                                                                                                                                                                                                          Fanger,
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Vedvick, Thomas S.
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                                                               Conservative
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                                                                                82.4%;
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Pred. No. 1.3e+02.
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Pred. No. 1.3e+02
                                                               Mismatches
                                                                                            DB 9;
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RESULT 7

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; ORGANISM: Pseudomonas aeruginosa US-09-815-242-5172
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                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
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Best Local Similarity 50...
"Thes 3; Conservative
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SEQ ID NO 1436
LENGTH: 95
TYPE: PRT
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                                                                                                                          NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 5172
LENGTH: 228
Query Match
Best Local Similarity
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CURRENT FILLING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-03-21
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APPLICANT: Steve Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
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ORGANISM: Homo sapiens
                                                                                                          TYPE: PRT
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Yamamoto, Robert T.
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82.4%;
50.0%;
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Pred. No. 1.4e+02;
Score 28; DB 10;
Pred. No. 3.1e+02;
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                  Length 228;
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APPLICANT: Cyskind, Judith
APPLICANT: Cyskind, John
APPLICANT: Trawick, John
APPLICANT: Forsyth, R. Allyn
APPLICANT: Forsyth, R. Allyn
APPLICANT: Forsyth, R. Allyn
APPLICANT: Forsyth, R. Allyn
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN
TITLE OF INVENTION: BECHERICHIA COLI
CURRENT APPLICATION NUMBER: US/09/912,020
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: 09/492,709
PRIOR APPLICATION NUMBER: 60/117,405
PRIOR APPLICATION NUMBER: 60/117,405
PRIOR APPLICATION NUMBER: 60/117,405
PRIOR FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 485
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH 233
TYDER: DET
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SOFTWARE: FastSEQ for Windov
SEQ ID NO 319;
LENGTH: 233;
TYPE: PRT
ORGANISM: Escherichia coli
US-09-741-669-319
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Best Local Similarity
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                                                                                                        US-09-912-020-386
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APPLICANT: Ohleen, Kari L.
APPLICANT: ZYSKIND, Judith W.
APPLICANT: ZYSKIND, Judith W.
TITLE OF INVENTION: Genes identified as required to the control of E. colones in the Experence: ELTERA.009A
CURRENT APPLICATION NUMBER: US/09/741,669
CURRENT FILING DATE: 2000-12-19
RIOR APPLICATION NUMBER: US 60/173005
PRIOR FILING DATE: 1999-12-23
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                                      Query Match
Best Local Similarity
                     Matches
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                                                                                                                     TYPE: PRT
ORGANISM: E. Coli
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                                      82.4%;
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: Pred. No. 3.2e
3; Mismatches
            3; Mismatches
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                                      Score 28; DB 10; Length 233; Pred. No. 3.2e+02;
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                   Indels
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US-09-815-242-13969
Sequence 13969, Application US/09815242
Patent No. US20020061569A1
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US-09-815-242-10353
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US-09-815-242-10353
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
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PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
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Best Local :
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        APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELLTRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
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TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
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APPLICANT: Zyskind, Judi
APPLICANT: Wall, Daniel
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PRIOR APPLICATION NUMBER: 60/191,078
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Yamamoto, Robert T.
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Pred. No. 3.2e+02;
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; ORGANISM: Helicobacter pylori
US-09-815-242-11592
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Query Match
Best Local Similarity
Thes 3; Conserve
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; Sequence 11592, Application

; Patent No. US20020061569A1
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
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NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 13969
LENGTH: 233
                                                                                                                                                               NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 11592
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PRIOR
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CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
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ORGANISM: Salmonella typhi
09-815-242-13969
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APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carr, Grant J.
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Zyskind, Judith W.
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                   Conservative
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50.0%;
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Pred. No. 3.2e
3; Mismatches
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               Score 28; DB 10; Length 234; Pred. No. 3.2e+02; Mismatches 0; Indels
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3.2e+02;
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APPLICANT:
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                                                                                                                                            APPLICANT:
                                              APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                      APPLICANT: NAKAGAWA, SATOSHI
                 CURRENT APPLICATION NUMBER: US/09/738,626
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ANDO, SEIKO
HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO

MIZOGUCHI, HIROSHI

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ORGANISM: Haemophilus influenzae
US-09-815-242-11103
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US-09-815-242-11103
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/21,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-28
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
US-09-738-626-3652
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SEQ ID NO 11103
LENGTH: 235
TYPE: PRT
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Best Local S
Matches 3
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TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
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Trawick, John
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Zyskind, Judith W.
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50.0%;
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1es 0;
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CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEO ID NOS: 7059
SOFTWARE: PATENTIN VET. 3.0
SEQ ID NO 3652
LENGTH: 293
TYPE: PAT
ORGANISM: Corynebacterium glutamicum
US-09-738-626-3652
Search completed: January 3, 2003, 15:52:06 
Job time: 4.77273 secs
                                                                                                                                                                                       Query Match 82.4%; Score 28; DB 9; Length 293; Best Local Similarity 50.0%; Pred. No. 3.9e+02; Matches 3; Conservative 3; Mismatches 0; Indels
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89 LQLWLF 94
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Title:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             al number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BLOSUM62
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38
1 WLVWIA 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    January 3, 2003, 15:21:45; Search time 26.5909 Seconds (without alignments) 30.067 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                908470 segs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A_Geneseq_101002:*

1. /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*

2. /SIDS2/gcgdata/geneseg/geneseqp-embl/AA1981.DAT:*

3. /SIDS2/gcgdata/geneseg/geneseqp-embl/AA1983.DAT:*

4. /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*

5. /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*

6. /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*

7. /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*

8. /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*
                                                                                                                            /SIDS2/gcgdatta/geneseq/geneseqp-embl/AA1992.DAT:*
/SIDS2/gcgdatta/geneseq/geneseqp-embl/AA1993.DAT:*
/SIDS2/gcgdatta/geneseq/geneseqp-embl/AA1994.DAT:*
/SIDS2/gcgdatta/geneseq/geneseqp-embl/AA1995.DAT:*
/SIDS2/gcgdatta/geneseq/geneseqp-embl/AA1995.DAT:*
/SIDS2/gcgdatta/geneseq/geneseqp-embl/AA1997.DAT:*
/SIDS2/gcgdatta/geneseq/geneseqp-embl/AA1998.DAT:*
                                                                                                                                                                                                                                                                                                                                                          /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

10	9	80	7	O	5	4	ω	2	1	Result No.
34	34	34	34	35	35	37	37	38	38	Score
89.5	89.5	89.5	89.5	92.1	92.1	97.4	97.4	100.0	100.0	Query Match Length DB
235	162	80	49	241	70	230	230	371	6	Length
22	22	22	23	23	22	22	22	23	23	i
AAU57493	AAU32492	AAM86002	ABG68706	ABP27890	AAU47680	AAB76811	AAG89817	ABB47793	AAU11850	ID
Propionibacterium	Novel human secret	Human immune/haema	Human prostate spe	Streptococcus poly	Propionibacterium	Corynebacterium gl	C glutamicum prote	Listeria monocytog	Peptide ligand for	Description

>

45	44			41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
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84.2	•	•	•																•	•			•	•	•	•			•	•	•	89.5		
153	153	153	149	139	128	115	105	95	89	84	75	32	735	504	497	472	396	362	362	329	296	185	185	171	171	162	145	132	95	78		676	2	288
21	21	21	22	13	15	20	23	21	22	23	21	20	22	22	20	22	22	17	15	22	22	21	21	21	21	21	22	22	23	22	21	20	22	22
AAG53000	AAG21898	AAG15863	AAM90245	AAR29009	AAR54053	AAY60396	ABP01702	AAG00323	AAO02795	ABP02429	AAB09351	AAY11779	AAU36496	ABG10850	AAY37610	ABG24925	ABG26161	AAW02667	AAR48695	AAB96276	AAG98330	AAG60773	AAG55839	AAG60774	AAG55840	AAG55841	AAU53601	ABG10849	ABP07995	AAO02505	AAB51390	AAY35418	AAU35667	AAU42440
Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia	Human immune/haema	p64-h2 protein pro	Sequence of the VL	Human normal bladd	Human ORFX protein	Human secreted pro	Human polypeptide	Human ORFX protein	Hepatitis GB virus	Human 5' EST secre	Pseudomonas aerugi	Novel human diagno	Protein which is s		Novel human diagno	G-protein coupled	ဂ္ဂ	Putative P. abyssi	coli					Arabidopsis thalia	ę.	Novel human diagno		ide	Human secreted pep	Chlamydia pneumoni	Haemophilus influe	Propionibacterium

## ALIGNMENTS

	PI H													AC A		RESULT 1 AAU11850
WPI; 2002-061944/08.	Hammond DJ, Wiltshire VR, Carbonell R, Shen H;	(VITE-) VI TECHNOLOGIES INC.	05-APR-2000; 2000US-0543188.	05-APR-2001; 2001WO-US11150.	18-OCT-2001.	WO200177687-A2.	Synthetic.	mionar maserny erocuse.	transmissible mink encephalopathy; exotic ungulate encephalopathy;	<pre>prion-associated disease; Creutzfeldt-Jakob disease; Gerstmann-Straussler-Scheinker disease; fatal familial insomnia;</pre>	Prion protein; Prp; ligand; octapeptide motif; scrapie;	Peptide liqand for Prion protein, PrP, #25.	26-MAR-2002 (first entry)	AAU11850;	AAU11850 standard; peptide; 6 AA.	1 50

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a ligand of less than 6 kD that binds to a polypeptide containing the sequence GlyTyrGlyValnProHisGlyGly (A) or an analogue that is the retro-inverso isomer of (A). The sequence A is an octapeptide motif from the prion protein (PrP). The ligands are identified by binding assays with the peptide (A) or peptides containing (A). The ligands are used for detecting prion proteins (or prions) in biological or environmental samples, e.g. for diagnosis, also for removing them from samples, for treating or retarding development of prion-associated diseases, specially Creutzfeldt-Jakob diseases (in latrogenic, new variant, familial or sporadic forms), but also cerstmann-Straussler-Scheinker disease, fatal familial insomnia, scrapie, bovine or feline spongiform encephalopathy, transmissible mink or exotic ungulate encephalopathy, or chronic wasting disease. The present sequence is a ligand of the invention.
                              Genomic sequence for Listeria and prevention of Listeria and related polypeptides -
                                                                                                        WPI;
                                                                                                                                                   Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P; Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P; Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A; Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L; Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
 Claim
                                                                                                                                      Perez-Diaz J, B
Maduenio E, De
Rose M, Voss H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin Bl2; bacterial infection; disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-FEB-2002
                                                                                                                                                                                                                                                                                                 (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                   11-APR-2000; 2000FR-0004629
                                                                                                                                                                                                                                                                                                                                                                     11-APR-2001; 2001WO-FR01118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Listeria monocytogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Listeria monocytogenes protein #497.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB47793 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 16; Page 34; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New ligands for prion proteins, useful for detection or removal or prions and for treating prion-associated diseases, recognize a specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 WLVWIA 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 WLVWIA 6
                                                                                                      2002-010914/01.
 6,
SEQ ID No 498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein;
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192pp; French
                                                    and
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Pred. No.
                                                  monocytogenes, useful e.g. for drelated bacterial infections,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 23;
.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                    for treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum.

These

SEQ ID NO: 3571; 246pp + Sequence Listing; English

Claim 17;

Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene

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RESULT 3
AAG89817
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Best Local S
Matches 6
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                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and modulate L. monocytogenes-related diseases. In addition, the gen sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections monocytogenes and related organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C glutamicum
                                                                  Nakagawa S,
Tateishi N,
                                                                                                                                                                                   03-AUG-2000;
                                                                                                                                                                                                                                                                              18-DEC-2000; 2000EP-0127688
                                                                                                                                                                                                                                                                                                                                                                                                                   Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                              organic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coryneform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note:
                                                                                                                                                                                                             07-APR-2000;
                                                                                                                                                                                                                                   16-DEC-1999;
                                                                                                                                                                                                                                                                                                                             20-JUN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG89817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              specification,
                                                                                                                                        (KYOW ) KYOWA HAKKO KOGYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG89817 standard; Protein; 230 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          313 WLVWIA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity hes 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Le: The sequence data for this patent did not form part of the printed
scification, but was obtained in electronic format directly from WIPO
ftp.wipo.int/pub/published_pct_sequences.
2001-376931/40.
DB; AAH65036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              orm bacterium; amino acid acid synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           371
                                                                  Mizoguchi
Senoh A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
                                                                                                                                                                                   2000JP-0159162.
2000JP-0280988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                   99JP-0377484
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                                                                                                                                                                                                                                                                                                                                                                                                                   glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fragment SEQ ID NO: 3571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100
                                                              H, Ando S, Hayashi M,
Ikeda M, Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 23;
1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23;
                                                                                          Ochiai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 371;
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RESULT 4
AAB76811
   ACC XXX ACC XX
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Matches
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25-JUN-1999
08-JUL-1999
08-JUL-1999
09-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and cryanic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corynebacterium glutamicum; brevibacterium lactofermentum; MCT; membrane construction and membrane transport protein; petroleum spill; hydrocarbon degradation; gram positive aerobic bacterium; marker; identification; microorganism; fine chemical production; transformation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200100805-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genome mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corynebacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            are useful for identifying the mutation point of a gene derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       170 WLIWIA 175
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5; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000WO-IB00926
               99DE-103229

99DE-1032212

99DE-1032227

99DE-1032228

99DE-1032230

99DE-1032927

99DE-1032927

99DE-1033005

99DE-1040764

99DE-1040765

99DE-1040766

99DE-1040766
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99DE-1032124.

99DE-1032125.

99DE-1032128.

99DE-1032180.

99DE-1032180.

99DE-1032190.

99DE-1032191.
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99DE-1031454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genetic engineering
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83.3%;
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Pred. No. 1.3e+02;
1; Mismatches (
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Matches 5
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31-AUG-1999;
31-AUG-1999;
31-AUG-1999;
03-SEP-1999;
03-SEP-1999;
03-SEP-1999;
03-SEP-1999;
               21-APR-2000;
02-JUN-2000;
07-JUL-2000;
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N-PSDB;
                                                                                                                            01-NOV-2001
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                                                                                        20-APR-2001;
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                                                                                                                                                                                                   Propionibacterium
                                                                                                                                                                                                                                        dermatological;
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les 5; Conserv
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               ; 2000US-199047P.
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; 2000US-216747P.
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AAF67743 to AAF68080 encode the Corynebacterium glutamicum membrane construction and membrane transport (MCT) proteins given in AAB76510 to AAB76847. The MCT nucleic acids and proteins are useful in the identification of microorganisms which can be used to produce fine chemicals, for modulating fine chemical production in C. glutamicum or related bacteria (e.g. Brevibacterium lactofermentum), the typing or identification of C. glutamicum or related bacteria, as reference points for mapping C. glutamicum genome, and as markers for transformation. AAF68082 and AAF68082 represent sequencing primers which are used in an example from the present invention.
                                                                                                                                                                                                                                             SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; Page 1012; 1119pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corynebacterium glutamicum nucleic acids encoding membrane construction and membrane transport proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers for transformation -
                                                                                                                                                                                                                                                                                                                                                              Propionibacterium acnes
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2001WO-US12865
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99DE-1041833.
99DE-1041378.
99DE-1041379.
99DE-1041395.
99DE-1042078.
99DE-1042078.
                                                                                                                                                                                                                         osteopathic;
                                                                                                                                                                  acnes.
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83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70
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Pred. No.
                                                                                                                                                                                                                         neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
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1.3e+02;
ches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 230;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cc polypeptides. The proteins and their associated DNA sequences are used in cc the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, the new proteins and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The cc polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and the conception of the sample, by can be used immunosorbent assay (ELISA).

CC specification, but was obtained in electronic format directly from WIPO can be used as antipolic for this patent did not format directly from WIPO can be used as obtained in electronic format directly from WIPO can be used as obtained in electronic format directly from WIPO can be used as obtained in electronic format directly from WIPO can be used as obtained in electronic format directly from WIPO can be used as obtained in electronic format directly from WIPO can be used as obtained in electronic format directly from WIPO can be used as obtained in electronic format directly from WIPO can be used as obtained in electronic format directly from WIPO can be used as obtained in electronic format directly from WIPO can be used as obtained in electronic format directly from WIPO can be used as obtained in electronic format directly from WIPO can be used as obtained to the used to 
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                                            27-OCT-2000;
24-NOV-2000;
07-MAR-2001;
                                                                                                                                             29-OCT-2001; 2001WO-GB04789
                                                                                                                                                                                            02-MAY-2002.
                                                                                                                                                                                                                                         WO200234771-A2
                                                                                                                                                                                                                                                                                     Streptococcus agalactiae
                                                                                                                                                                                                                                                                                                                                  Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus polypeptide SEQ ID NO 4956.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABP27890;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP27890 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
(CHIR-) CHIRON SPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L'maisonneuve
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DB; AASS9539.
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                                            ; 2000GB-0026333.
; 2000GB-0028727.
; 2001GB-0005640.
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e J, Zhang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 35; DB Pred. No. 78; 1; Mismatches
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RESULT 7
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Best Local Similarity
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Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus/GAS (Streptococcus/GAS (Streptococcus yyogenes), comprising one of $483 sequences ($1), given in the specification. The proteins have antibacterial and antinfilammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71326 and antibacteriathat bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds to biological sample. (I) is used to determine whether a compound binds to used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic statics of the streptococcus that is prevented or treated may be meningitis. Nucleic contains of the streptococcus of the s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; prostate specific nucleic acid; PSNA; prostate cancer; PSP; prostate specific protein; cytostatic; non-cancerous prostate disease;
WPI; 2002-557831/59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human prostate specific protein DEX0293_75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-OCT-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 3656; 4525pp; English.
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                                                                                                                                                                                                                                                                                                                                        27-NOV-2000; 2000US-253176P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a protein (ABP25413-ABP30895) from group B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ABN68521.
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                                                                                          S, N
                                                                                                                                                                                                                                             DIADEXUS INC
                                                                                          Macina RA,
n S;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer; immunostimulant; vaccine.
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83.3%;
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Pred. No. 2.8e+02;
Pred. No. 2.8e+02;
                                                                                                                                        Cafferkey R,
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RESULT 8
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Matches 4; Conserv
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   31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
11-MAR-2000;
11-MAR-2000;
11-MAR-2000;
11-MAY-2000;
07-JUN-2000;
07-JUN-2000;
07-JUN-2000;
07-JUL-2000;
07-JUL-2000;
07-JUL-2000;
07-JUL-2000;
07-JUL-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnosing and monitoring the presence and metastases of prostate cancer in a patient (the kit for detecting a risk of cancer or presence of cancer in a patient (the kit comprising a means for determining the presence of the PSNA or PSP in a sample of a patient) and a vaccine comprising the polypeptide or the nucleic acid encoding the polypeptide. The PSNA, PSP and anti-PSP antibody are useful for diagnosing and treating cancer in a patient (e.g. by gene therapy). The nucleic acid molecule and polypeptide are also useful as vaccines for treating cancer, particularly prostate cancer and non-cancerous prostate diseases. The present sequence is a PSP of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a new isolated prostate-specific nucleic acid (PSNA) molecule comprising the CDNA sequences appearing as ABK97574-ABK97642 which encode prostate specific proteins appearing as ABK97574-ABK97646, or a sequence hybridising to a PSNA or which has 60% sequence homology with a PSNA. Also included are a method of determining the presence of a PSNA in a sample, a vector comprising the PSNA, a host cell comprising the vector, producing the polypeptide encoded by a host cell comprising the vector, producing the polypeptide encoded by the PSNA, a method of determining the presence of a PSF in a sample,
                                                                                                                                                                                                                                                    17-JAN-2001;
                                                                                                                                                                                                                                                                                    09-AUG-2001
                                                                                                                                                                                                                                                                                                                   WO200157182-A2
                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                   cytostatic; gene therapy; vaccine; metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                 Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immune/haematopoietic antigen SEQ ID NO:13595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Page 192; 212pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New prostate specific genes, useful for treating or diagnosing cancer, or useful as vaccines for treating cancer, particularly prostate cancer, in a patient \, -
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   2000US-0179065

2000US-0186628

2000US-0184664

2000US-0186350

2000US-018974

2000US-0199123

2000US-0199123

2000US-0205467

2000US-0215135

2000US-0215647

2000US-02156847

2000US-0216880

2000US-0216880

2000US-0216880
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Pred. No.
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77;
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     14-AUG-2000
18-AUG-2000
18-AUG-2000
22-AUG-2000
23-AUG-2000
23-AUG-2000
23-AUG-2000
01-SEP-2000
01-SEP-2000
01-SEP-2000
06-SEP-2000
06-SEP-2000
08-SEP-2000
08-SEP-2000
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01-SEP-2000
01-SEP
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14-AUG-2000;
14-AUG-2000;
2000US-022924

2000US-0229343

2000US-0229343

2000US-0229509

2000US-0229509

2000US-0229509

2000US-0231243

2000US-0231243

2000US-0231413

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2000US-0231413

2000US-0231413

2000US-02312081

2000US-0232081

2000US-02323081

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2000US-02323081

2000US-02323063

2000US-0233063

2000US-0232401

2000US-0233063

2000US-0234997

2000US-0235834

2000US-0235836

2000US-0236369

2000US-0237037

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2000US-02341786

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2000US-0225759.
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2000US-0226681.
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2000US-0227182.
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2000US-0225213.
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2000US-0225447.
2000US-02254757.
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2000US-0218290.
2000US-0220963.
2000US-0220964.
2000US-0224518.
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33333333<del>%</del>&

protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoletic-related diseases, especially cancers and cancer metastases of haematopoletic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoletic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169

sequences used in the exemplification of the present invention

the nucleic acids into a host cell and culturing

the cell to express the

В Š

61 WLLWVA 66

1 WLVWIA 6

Matches Query Match Best Local

4;

Conservative

Local Similarity

89.5%;

Score Pred.

Mismatches 34;

Indels 80

0;

Gaps

0

1.3e+02; 0;

Length

Sequence

80 AA;

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01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
                                    AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis are treatment of diseases associated with inappropriate (I) expression. For
                                                                                     Claim 11;
                                                                                                   useful for preventing, metastasis -
                                                                                                                 Nucleic acids encoding
                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                           17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                        17-NOV-2000;
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DB; AAK58783.
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2000US-0256719
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                                                                                  NO 13595; 3071pp + Sequence Listing; English
                                                                                                                                                        SC,
                                                                                                                                                        MS
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example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting human immune/hematopoietic antigen polypeptides, diagnosing and/or treating cancers and decreased and The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and the useful in genetic vaccination, testing and the useful in genetic vaccination, testing and the useful the proteins are useful in genetic vaccination. therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopolesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention. Claim Nucleic acids encoding a range of vaccination, testing and therapy Tang Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia WPI; 2001-611725/70 18-APR-2000; 26-JAN-20**0**1; 16-APR-2001; 2001WO-US08656 WO200179449-A2 18-DEC-2001 (HYSE-) HYSEQ INC Homo sapiens. Novel human secreted protein #2983 AAU32492 standard; Protein; 162 YT, 20; Page 623; 765pp; English. Liu C, 2000US-0552929. 2001US-0770160. (first entry) Drmanac range of human polypeptides, useful in genetic RT

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Best Local
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                                                                                                                          polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to compression and activities of P. acnes antigens are polypeptides.
               at ftp.wipo.int/pub/published_pct_sequences
                              Note: The sequence data for this patent did not form specification, but was obtained in electronic format
                                                                 enzyme
                                                                          downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used diagnostic agents for determining P. acnes presence, for example, by
                                                                                                                                                                                                                                                                                                                                                                       Example 1; SEQ ID No 18688; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                          treating acne vulgaris
                                                                                                                                                                                                                                                                                                                                                                                                                            vaccinating against and
                                                                                                                                                                                                                                                                                                                                                                                                                                            Propionibacterium acnes
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02-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Propionibacterium acnes immunogenic protein #18389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
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                                                            linked immunosorbent assay (ELISA)
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                                                                                                                                                                                                                                                                                                                     AAU39105-AAU68017 represent Propionibacterium acnes des. The proteins and their associated DNA sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; 2000US-199047P.
; 2000US-208841P.
; 2000US-216747P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptides and nucleic acids useful for diagnosing infections, especially useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Υ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mitcham JL, Wang SS, Jen S, Carter D;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                              part of the printed directly from WIPO
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                                                                                                                                                                                                                                                                                                                       immunogenic
are used in
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RESULT 11
AAU42440
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Best Local S
Matches 5
             specification, at ftp.wino in
                                                             and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).
                                                                                                                                                                                       pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                             Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Skeiky YAW, Persing L'maisonneuve J, Zha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-APR-2000; 2000US-199047P.
02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAPHO syndrome; synovitis; acne; uveitis; endophthalmitis; bone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU42440;
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                                                                                                                                                                                                                                                                                                    P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
                                                                                                                                                                                                                                                                                                                   polypeptides. The proteins and their associated DNA sequences are use the treatment, prevention and diagnosis of medical conditions caused
                                                                                                                                                                                                                                                                                                                                                                                          Example 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                              treating acne vulgaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-APR-2001; 2001WO-US12865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Propionibacterium acnes immunogenic protein #3336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 WLVWIA 6
                                                                                                                                                                                                                                                                                                                                      {\tt AAU39105\text{-}AAU68017} represent Propionibacterium acnes immunogenic des. The proteins and their associated DNA sequences are used in
                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID No 3635; 1069pp; English
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              .int/pub/published_pct_sequences
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, Jen S, Carter D;
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Pred. No.
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3.9e+02;
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AAU35667
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Best Local Similarity
Matches 5; Conserv
                         invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent din of form part of the printed specification, but was obtained in electronic format directly from MIPO at
                                                                                                                                                                                                                    The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
                                                                                                                                                                                                                                                                                                                                                                   New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
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23-MAY-2000; 2000US-206848P.
26-MAY-2000; 2000US-207727P.
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                                                                                                                                                                                                                                                                                                                                    Example 3; Seq ID No 11260; 511pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haselbeck R,
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27-NOV-2000;
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             .wipo.int/pub/published_pct_sequences
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2000US-242578P.
2000US-253625P.
2000US-257931P.
2001US-269308P.
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Xu HH;
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Pred. No. 4.8e+02;
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RESULT 14 AAB51390 ID AAB5

AAB51390 standard;

Peptide;

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                                                                                                        RESULT 13
AAY35418
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                                                                                                                            AAY34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see AAX91990) of Chlamydia pneumoniae. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                   Genome sequence of Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                WPI; 1999-357842/30
                                                                                                                                                                                                                                                                                                                                                                                                                            04-NOV-1998;
21-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chlamydia pneumoniae cellular envelope protein
                                                                                                                                                                                                                                                                                         Page 1199-1201; Disclosure; 1912pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-JUN-1999
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481 WLVWI 485
                                                   Local Similarity tes 5; Conserv
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les 5; Conserv
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                                                                                                        676 AA;
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97FR-0014673
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                                                               89.5%;
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                                                               Score 34; pred. No.
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                                                   Mismatches
                                                               DB 20;
. 1.1e+03;
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7e+02;
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                                                                                                                                  RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequences AAB51380-B51423 represent the amino acid sequences of 45 human secreted proteins encoded by the genes AAC93310-C93354. The genes and proteins are useful for preventing, ameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and overlan cancer, and other cancers of the adorenal gland, bone, bone marror breast astroitestical tract
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytostatic; immunosuppressive; nootropic; neuroprotective; antivaler; antialergic; hepatotropic; antidiabetic; antiinflammatory; antiparasitic; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; vulnerary; haranv: cancer; immune disorder; cardiovascular disorder;
Human polypeptide SEQ ID NO 16397.
                                  06-NOV-2001
                                                                                                 AAO02505 standard; Protein;
                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                              epilepsy; and and parasitic
                                                                                                                                                                                                                                                                                                                                                                                                  colitis;
                                                                                                                                                                                                                                                                                                                                                                                                              marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, altergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid molecules encoding 45 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB;
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07-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cardiant; gene therapy; cancer; immune disorder; cardicvaneurological disease; infection; human; secreted protein.
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                                                                                                                                                                                                                                                                                                                                                            colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, funga.
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DB; AAC93320.
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                                (first entry)
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2000US-0174847.
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                                                                                                                                                                                                                  Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immundisorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; cytokine; cell proliferation; cell differentiation; gene thy vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cencer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to human polynucleotides (AAI79941-AAI93841) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
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# ALIGNMENTS

#### probable membrane protein lin0925 [imported] - Listeria innocua (strain Clip11262) C;Species: Listeria innocua C;Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 27-Nov-2001 C;Accession: AE1548 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Blc.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsil D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001 A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, & Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wel A;Filtle: Comparative genomics of Listeria species. A;Reference number: AB1077; MUID:21537279; PMID:11679669 A; Experimental source: strain EGD-e C; Genetics: D; Jones, L.M.; Karst, U. Science 294, 849-852, 2001 Science 294, 849-852, 2001 A; Authors: Kreft, J.; Kuln, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; A;Title: Comparative genomics of Listeria species. A;Reference number: AB1077; MUID:21537279; PMID:11679669 A;Accession: AE1190 probable membrane protein lmo0925 [imported] - Listeria monocytogenes (strain c;Specles: Listeria monocytogenes C;Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 27-Nov-2001 C;Accession: AE1190 C;Accession: AE1190 C;Accession: AE1190 C;Accession: AE1190 C;Accession: Dichaud, E; Buchrieser, C; Amend, A; Baquero, F; Berche, P.; Dominguez-Bernal, G; Duchaud, E; Durand, L; Dussurget, O; Entian, K.D.; Jones, L.M.; Karst, U. A; MOJecule type: DNA A; Residues: 1-371 <GLA> A; Cross-references: GB: AL592022; PIDN:CAC96157.1; PID:g16413373; A; Experimental source: strain Clip11262 A;Reference number: AB1077; A;Accession: AE1548 A;Status: preliminary RESULT AE1548 DЪ Qγ A; Molecule type: DNA A; Residues: 1-371 <GLA> A; Cross-references: GB: A; Gene: A; Status: preliminary Query Match Best Local Matches 313 1 WLVWIA 6 1mo0925 WLVWIA 318 Similarity 6; Conser Conservative 100.0%; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P. chaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; 0; Score 38; DB Pred. No. 45; Mismatches PIDN:CAC99003.1; PID:g16410327; GSPDB:GN00177 DB 45; 2: 0; Length 371; Indels . . Berche, P.; Gaps Maitournam, A.; Voss, H.; Wehla Maitournam, Voss, H.; W 0; EGD-e) ; Bloec Fsihi, ; Bloec Fsihi, m, A.; Wehla

GSPDB: GN00178

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Nakazaki, N.; Shimpo, S.; Sugimoto, M., Almander.
Nakazaki, N.; Shimpo, S.; Sugimoto, N., Almander.
Nakazaki, N.; Shimpo, 
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C; Accession: AF2493
R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, SR; Kaneko, N.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, SR; Kaneko, M.; Yamada, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada,
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A:Residues: 1-719 <KUSA
A:Cross-references: GB:AE006469; PIDN:AAK65164.1; PID:g14523607; GSPDB:GN00165
A:Experimental source: strain 1021, megaplasmid pSymA
A:Experimental source: strain 1021, megaplasmid pSymA
R:Gallbert, F: Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L: Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
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Pitle: Nucleotide sequence and predicted functions of the entire Sinorhizobium K;Reference number: A99262; MUID:21396509; pMID:11481432
A;Accession: B95325
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             conserved hypothetical protein SMa0937 [imported] - Sinorhizobium meliloti (strain
c;Specles: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: B95325
                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-651 <KUR>
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A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp.
C;Date: 14-Dec_2001 #sequence_revision 14-Dec-2001 #text_change
                                                                                                                                                         A; Experimental source: strain PCC
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A;Gene: lin0925
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.48;
83.38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 37; DB
Pred. No. 1.1e
1; Mismatches
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Le..
. 1.1e+02;
. cos 0;
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45;
                                                                                                                                                                                              PID:g17135664; GSPDB:GN00180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S.; ¥
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30-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Watanabe, A.; ; Yasuda, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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K.C.
RESULT
S73854
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WLLWIA 14

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A; Map position: 4
A; Introns: 36/1; 74/2; 100/1;
C; Superfamily: Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-536 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, A;Reference number: Z19317 A;Accession: T20736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Species: Caenorhabditis elegans
C; Date: 15-Oct-1999 #sequence_rev:
C; Accession: T20736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;
A;Title: Complete genome sequence of a multiple drug resistant
A;Reference number: ABOS02; PMID:11677608
A;Accession: ADOS21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable symporter STY0171 [imported] - Salmonella enterica subsp. enterica serovar T C; Species: Salmonella enterica subsp. enterica serovar Typhi A; Note: this species has also been called Salmonella typhi C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001 C; Accession: AD0521 C; Called Salmonella typhi C; Accession: AD0521 C; Called Salmonella typhi C; Control C; Accession: AD0521 C; Called Salmonella typhi C; Called Salmonella enterica serovar Typhi C; Called Salmonella typhi C;
                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:268297; PIDN:CAA92595.1; GSPDB:GN00022; CESP:F11A10.5 A;Experimental source: clone F11A10
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T20736
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A;Molecule type: DNA
A;Residues: 1-468 <PAR>
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C;Superfamily: melibiose
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein F11A10.5 - Caenorhabditis elegans
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                                                           Matches
                                                                                        Query Match
Best Local
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Best Local :
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Best Local
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WLVWIA 6
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5; Conserv
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                                                               Conservative
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                                                                                     92.1%;
83.3%;
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83.3%;
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                                                                                                                                                                                157/1; 237/1; 269/3; elegans hypothetical
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Pred. No. 1.5e
1; Mismatches
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Pred. No.
                                                                                        Score 35;
Pred. No. 1
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                                                               Mismatches
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ches 0;
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1.5e+02;
                                                  .8e+02;
0;
                                                                                                                    DB 2;
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protein F11A10.5
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                                                                                                                 Length 536;
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                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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Salmonella enterica
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                                                        0:
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                                                        Gaps
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                                                        0;
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A;Title: The complete genome A;Reference number: A70300; NA;Accession: E70473
                                                                                                                                                                                                          phosphate transport system permease PstA - Aquifex aeolicus
C;Species: Aquifex aeolicus
C:Date: 08-May.1998 #sequence_revision 08-May-1998 #text_ch
C;Accession: E70473
                                                                                                                                                                                                                                                                                              RESULT
E70473
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T19814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein C38C6.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Decies: Caenorhabditis elegans
C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 17-Mar-2000
C;Accession: T19814
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A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma A;Reference number: S73327; MUID:97105885; PMID:8948633
A;Accession: S73854
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Mycoplasma pneumoniae
A;Variety: ATCC 29342
C;Date: 27-Feb-1997 #sequence_revision 25-Apr-1997
A;Cross-references: GB:AE000768; NID:g2984249; PIDN:AAC07781.1; PID:g2984254; GB:AE00069
                       A; Molecule type: DNA
A; Residues: 1-285 < AQF>
                                                            A; Status: preliminary; nucleic acid
                                                                                                                                                                                      R;Deckert, G.; Warren, P.V.; Gaasterland, T.;
                                                                                                                                                                                                                                                                                                                                                                             Вр
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A; Introns: 17/2; 97/2;
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                                                                                                                                                  Nature 392, 353-358, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: CESP:C38C6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:Z93375; PIDN:CAB07562.1; GSPDB:GN00020; CESP:C38C6.2
A;Experimental source: clone C38C6
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A; Residues: 1-585 <WIL>
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A; Residues: 1-565 <HIM>
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10rosidase; alpha-amylase core homology
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66.7%;
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66.7%;
                                                                                                     of the hyperthermophilic bacterium Aquifex aeolicus MUID:98196666; PMID:9537320
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Pred. No. 1.9e+02;
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                                                                not shown;
                                                                                                                                                                                      Young, W.G.; Lenox,
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                                                                                                                                                                                                                             #text_change 26-Aug-1999
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RESULT 10
G72310
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C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: G72310
Вb
                                                                                                                                                                                                                                                                                                                  acyltransferase homolog [imported] - Mycobacterium C;Species: Mycobacterium leprae C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 C;Accession: T44870
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C;Superfamily: phoW
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                                                                                                                        A; Note: MLCB1883.06
C; Superfamily: 4''-(
                                                                                                                                                           C; Genetics:
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A;Experimental source: cosmid B1883
                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-384 < PAR>
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A;Cross-references: GB:AE001760; GB:AE000512; NID:g4981510; PIDN:AAD36065.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hi
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
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WIVWLA 125
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5; Conser
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5; Conser
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the EMBL Data Library, April
                                                                                                                        4''-0-acyltransferase
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Pred. No.
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Pred. No. 1.6e+02;
0; Mismatches 1;
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Pred. No. 1.5e+02;
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hypothetical protein AT4903490 [imported] - Arabidopsis thaliana C:Species: Arabidopsis thaliana (mouse-ear cress) C:Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001 C:Accession: C85044 R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana. A;Reference number: A85001; MUID:20083488; PMID:10617198
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C85044
                                                                                                      A; Molecule type: DNA
A; Residues: 1-703 <ARN>
                                                                                                                                                                                       R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206606; PMID:10192388
A;Accession: H72034
                                                                                                                                                                                                                                                                                                                                   thiol-disulfide interchange protein dsbD [imported] - Chlamydophila pneumoniae C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 28-Jul-2000 C;Accession: H72034
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A;Authbors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: A64132
                                                    A; Experimental source:
                                                                           A;Cross-references: GB:AE001660; GB:AE001363; NID:g4377095; PIDN:AAD18924.1; PID:g43770
                                                                                                                                                                A; Status: preliminary
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A; Residues: 1-587 <STO>
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C;Accession: A64132
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                    Genetics:
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A;Title: Comparison of whole genome sequences of chlamydia pneum A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Accession: H85588
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Search completed: Job time: 10.9545
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                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-703 <STO>
                                                                                                                                                                                                                                                                                                                                                                                      thio,disulfide interchange protein [imported] - Chlamydophila pneumoniae (strain J138 C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001 C;Accession: H86588
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petunia hyb
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                                                                                                                  Hypothetical TRANSMEM
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[1]
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                                                                                                                                         InterPro;
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VGL2_IBVK	VGL2_IBVB	VGL2_IBVD2	BOSS_DROME	TLR2_MACFA	TLR2_HUMAN	MAE1_SCHPO	TRI5_MYRRO	TRI5_STACH	TRI5_GIBPU	G392_DROME	TRI5_FUSPO
P12650 avian infec	P11223 avian infec	P12722 avian infec	P22815 drosophila	Q95m53 macaca fasc		P50537 schizosacch	Ol3489 myrothecium		P27679 gibberella	P58957 drosophila	Q00835 fusarium po

# ALIGNMENTS

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TRANSMEM
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P75472; 008088;

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence updat

16-OCT-2001 (Rel. 40, Last annotation upon

Hypothetical protein MPN308 (F10_orf565).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pneumoniae cytoskeletal protein HMW2 and cytadherence.";

J. Bacteriol. 179:2668-2677(1997).

-i- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

-i- SIMILARITY: IN THE N-TERMINAL SECTION; TO M.PNEUMONIAE MPN095.

-i- SIMILARITY: IN THE C-TERMINAL SECTION; TO M.PNEUMONIAE MPN096.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRALN-ATCC 29342 / M129;
MEDLINE=97105885; PubMed=8948633;
Himmelreich R., Hilbert H., Plagens H.,
                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE000052; AAB96176.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97252497; PubMed=9098066;
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Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
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Best Local Similarity
Matches 5; Conserv
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16-OCT-2001
16-OCT-2001
16-OCT-2001
                     YG04_HAEIN STANDARD; PRT; 420 AA. P45268; O1-NOV-1995 (Rel. 32, Created) O1-NOV-1995 (Rel. 32, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
            Putative
                                                                                                                                                                                                                                                                            EMBL; AE001760; AAD36065.1; -.
TIGR; TM0986; -.
Hypothetical protein; Complete
SEQUENCE 318 AA; 36705 MW;
                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-MSBB / DSM 3109;

MEDLIND-99287316; PubMed=10360571;

Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.

Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson

Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O

Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

"Evidence for lateral gene transfer between Archaea and Bacteria
genome sequence of Thermotoga maritima.";

Nature 399:323-329(1999).

"I-SIMILARITY: STRONG, TO E.COLI YFAT AND P.AERUGINOSA PA4490.
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            phosphate
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482
516
565
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(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
1 protein TM0986.
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Pred. No. 65;
2; Mismatches
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Pred. No.
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ACC745B43D2184E2 CRC64;
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7041AB7510531380 CRC64;
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57;
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Best Local
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                               01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ATP synthase B' chain (EC 3.6.3.14) (Subunit
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Cyanophora Cyanelle.
                       ATPG.
                                                                                 P48085;
                                                                                            ATPX_CYAPA
                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U32834; AAC23248.1; TIGR; HI1604; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on if
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Science 269:496-512(1995).
Science 269:496-512(1995).
--- mombrane prote:
                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-Rd / KW20 / MEDLINE-95350630;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein; Phosphate transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO THE PHO-4 FAMILY OF TRANSPORTERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haemophilus influenzae
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5; Conserv
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420 AA;
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Conservative
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PubMed=7542800;
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Pred. No.
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15-JUN-2002 (Rel. 41,
15-JUN-2002 (Rel. 41,
15-JUN-2002 (Rel. 41,
Phosphate transport s
PSTA OR YPO4115.
STRAIN=CO-92 / Biovar Orientalis; MEDLING=21470413; PubMed=11586360; Parkhill J., Wren B.W., Thomson N.R., T. Prentice M.B., Sebaihia M., James K.D., Baker S., Basham D., Bentley S.D., Brool
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Loeffelhardt W., Stirewalt V.L., Michalowski C.B., Annarella Farley J.Y., Schluchter W.M., Chung S., Newmann-Spallart C., Steiner J.M., Jakowitsch J., Bohnert H.J., Bryant D.A.; "The complete sequence of the cyanelle genome of Cyanophora the genetic complexity of a primitive plastid."; (In) Schenk H.E.A., Herrmann R., Jeon K.W., Mueller N.E., Schwerter W. C.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B FOUND IN PLANTS AND PHOTOSYNTH
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NCBI_TaxID=2762;
                                                                        SEQUENCE FROM N.A.
                                                                                                    NCBI_TaxID=632;
                                                                                                                                Yersinia pestis.
Bacteria; Proteobacteria;
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3; Conserv
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ransport system permease protein p
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                                                                                                                                                                                                                                              STANDARD;
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50.0%;
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13:327-332(1995).
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TP + H(2)O + H(+)(In) = P
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3; Mismatches
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                                                                                                                                subdivision;
    Brooks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Springer-Verlag,
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  Titball R.W., Holden M.T.G., ., Churcher C., Mungall K.L., ooks K., Cerdeno-Tarraga A.M.
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45;
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01-APR-1988
15-JUN-2002
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            MEDLINE=85104705; pubMed=3881386;
Surin B.P., Rosenberg H., Cox G.B.;
"Phosphate-specific transport system of Escherichia
sequence and gene-polypeptide relationships.";
J. Bacteriol. 161:189-198(1985).
                                                                                               SEQUENCE FROM N.A.
MEDILINE-85293094; PubMed-2993631;
Amemura M., Makino K., Shinagawa H., Kobaya
"Nucleotide sequence of the genes involved
regulation of the phosphate regulon in Esch
J. Mol. Biol. 184:241-250(1985).
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between
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Escherichia
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Transport, Phosphate transport; Transme
Complete proteome
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TIGRFAMs; TIGR00974; 3a0107s02c;
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SIMILARITY: BELONGS TO THE BIN
SYSTEM PERMEASE FAMILY. CYSTW
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sen the Swiss Institute of Bioinformatics and the EMBL outstation -
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295 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Burland V.D., Plunkett G. III, Daniels D.L., Blattner F.R.; "DNA sequence and analysis of 136 kilobases of the Escherichia coligenome: organizational symmetry around the origin of replication."; Genomics 16:551-561(1993).
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"Mutational analysis of the Escherichia coli phosphate-specific transport system, a member of the traffic ATPase (or ABC) family membrane transporters. A role for proline residues in transmembra
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MEDLINE-93315143; PubMed-7686882;
Burland V.D., Plunkett G. III, Da
                                                                                                                                                                                                              SEQUENCE
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TIGRFAMS; TIGR00974; 3a0107s02c; 1.
PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; 1.
Transport; Phosphate transport; Transmembrane; Inner membrane;
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                                                                                                                                                                           Local Similarity
                                                                                                                                     1 WLVWI
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SUBCELULIAR LOCATION: Integral membrane protein. Inner membrane.
SIMILARITY: BELONGS TO THE BINDING-PROTEIN-DEPENDENT TRANSPORT
SYSTEM PERMEASE FAMILY. CYSTW SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3101. Chem. 267:24661-24668(1992).
EUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT FOR PHOSPHATE: PROBABLY RESPONSIBLE FOR THE TRANSLOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     K01992; AAA24380.1;
L10328; AAA62077.1;
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09TL07;

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

15-Jun-2002 (Rel. 41, Cast annotation update)
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"Complete sequence and gene organization of the genome of a hyper-thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
                                                     Eukaryota; Viridi
Chlorodendrales;
NCBI_TaxID=31312;
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                    SEQUENCE FROM N.A.
STRAIN=NIES-484;
                                                                                          Nephroselmis olivacea. Chloroplast.
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         MEDLINE=99398694; PubMed=10468594;
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Otis C.,
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P40550; Q03092;
01-FEB-1995 (Rel. 31, Created)
01-CCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                   Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D., Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D., Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V., Walsh S.V., Whitehead S.; Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
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             Decottignies A., Lambert L., Catty P., Degand H., Epping E.A., Moye-Rowley W.S., Balzi E., Goffeau A.; "Identification and characterization of SNQ2, a new multidrug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oxidoreductase; TRANSMEM 15
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                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; / Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
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                                                                   MEDLINE=95355421; PubMed=7629127
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                                                                                         [DENTIFICATION,
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p15733;
01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence up
01-APR-1990 (Rel. 14, Last annotation
Hypothetical 4.6 kDa protein (ORF1).
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STRAIN-ATCC 27894 / UTEX 581;
Wickrema A., Barnum S.R., Jaworski J.G.;
Submitted (JAN-1989) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; 238113; CAA86236.1; -. EMBL; Z46881; CAA86980.1; -. SGD; S0001275; PDR11.
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PROSITE; PS00211; ABC_TRANSPORTER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
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This SWISS-PROT entry is copyright.
                                                                             Bacteria; Cyanobacteria;
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01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Mercuric transport protein (Mercury ion trans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shewanella putrefaciens (Pseudomonas putrefaciens).
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PIR; S08038; S08038.
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                                                                                                                                                                                                                                                                                                                                           FUNCTION: INVOLVED IN MERCURIC TRANSPORT. PASSES A \mathrm{HG}(2+) FROM THE PERIPLASMIC MERP PROTEIN TO THE MERCURIC REDUCTAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pean Bioinformatics Institute. There are no restrictions non-profit institutions as long as its content is in and this statement is not removed. Usage by and for contents are not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proteobacteria;
                                                                                                                                                                                IPR003457;
                                                  10
45
92
23
24
75
81
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       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PMERPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein; Plasmid
) AA; 4592 MW; {
                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                            operon
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65
112
23
24
75
                                                                                                                                                         resistance;
                                                   12555
               84.2%;
                                                                                                                                                                                                                                                                                                                                                                  19:239-262(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84.2%;
80.0%;
                                                                                                                                                                              Transprt_MerT.
                                                   ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gamma subdivision; Alteromonadaceae;
       <u>ب</u>
                                                 POTENTIAL.
POTENTIAL.
POTENTIAL.
HG(2+) (BY SIMILARITY).
                 Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 32;
Pred. No.
                                                                                                                                                                                                                                                                        of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83D6BFDB296D7D37
                                                                                                                                 POTENTIAL.
                                                                                                                                                        Inner membrane;
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        рв
19;
                 48;
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                            DΒ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transport protein).
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bacterial mercury
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                           Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and the
                                                   CRC64;
                                                                                                                                                                                                                                                                         and the
                                                                                                                                                        Mercury; Plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
       Indels
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                                                                                                                                                                                                                                                                                                                      Inner membrane.
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Query Match
Best Local S
Matches 4
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30-MAY-2000 (Rel. 3
30-MAY-2000 (Rel. 3
15-JUN-2002 (Rel. 4
ER lumen protein re
                                                                                  DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Guyon V.N., Astwood J.D., Garner E.C., Dunker A.K., Taylor L.P., "Isolation and characterization of cDNAs expressed in the early stages of flavonol-induced pollen germination in petunia.", Plant Physiol. 123:699-710(2000).

-i- FUNCTION: REQUIRED FOR THE RETENTION OF LUMINAL ENDOPLASMIC RETICULUM PROTEINS, DETERMINES THE SPECIFICITY OF THE LUMINAL PROPEIN RETENTION SYSTEM. ALSO REQUIRED FOR NORMAL VESICULAR PROPEIN RETENTION SYSTEM. ALSO REQUIRED FOR NORMAL VESICULAR TRAFFIC THROUGH THE GOLGI. THIS RECEPTOR RECOGNIZES H-D-E-L (TRAFFIC THROUGH THROU
                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Viridiplantae; Streptophy Spermatophyta; Magnoliophyta; eudicc Asteridae; euasterids I; Solanales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ERD2_PETHY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF049922; AAD02548.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20317212; PubMed=10859200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Petunia hybrida (Petunia).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO THE ERD2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |:|| |
  Similarity
4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PD005774;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F00810; ER_lumen_recept; PR00660; ERLUMENR.
                                                                                                                                                                                                                                                                                                                                                                                                                                      PS00952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS00951;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein retaining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR000133; ERret_receptor
                                                                                    215
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    Conservative
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                                                                                                                                                                                                                                                   36
54
62
99
                                                                                    AA;
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39,
41,
                                                                                                                                                                                                                                                                                                                                                                                                                                ERret_receptor; 1.
ER_LUMEN_RECEPTOR_1; 1.
                     84.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
Lining receptor (HDEL receptor) (PGP169-12).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptophyta; Embryophyta; Tracheophyta yta; eudicotyledons; core eudicots;
                                                                                    MW.
                   Score 32;
Pred. No.
                                                                                  CYTOPLASMIC (POTENTIAL). 7A6E4EF4F017CF65 CRC64;
                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                  POTENTIAL
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  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Solanaceae;
                                                                                                                                                                                                                                                                                                              (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                               Protein transport;
                         83;
                                          DB
                                        Length 215;
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      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                 Receptor.
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Вp

181 WITWIA

186

AQPZ\_BRUAB RESULT 13

STANDARD;

PRT;

228

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Вр
                                                          Query Match
Best Local
                                               Matches
                                                                                              DOMAIN
SEQUENCE
                                                                                                                                                       TRANSMEM
REPEAT
                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Microbiology 146:3251-3257(2000).
-!- FUNCTION: Transport of water across the membrane. Possibly involved in the adaptation to variation in intravacuolar pl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brucella abortus.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9LA79;
15-JUN-2002
                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                           Transport;
                                                                                                                                                                                                                                                                     TIGRFAMS;
                                                                                                                                                                                                                                                                              PRINTS; PR00783; MINTRINSICP. ProDom; PD000295; MIP_family; 1.
                                                                                                                                                                                                                                                                                                        Pfam; PF00230; MIP;
                                                                                                                                                                                                                                                                                                                               EMBL; AF148066; AAF73105.1; -. HSSP; P29972; 1H6I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-2308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brucellaceae; Brucella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQPZ OR AQPX
                                                                                                                                                                                  TRANSMEM
                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brucella abortus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rodriguez M.C., Froger A., Rolland J.-P., Thomas Delamarche C., Garcia-Lobo J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20553188; PubMed-11101683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aquaporin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQPZ_BRUAB
                                                                                                                                                                                                          RANSMEM
                                                                                                                                                                                                                                                                                                                     nterPro;
204
                                             Local Similarity
nes 4; Conserv
                      1 WLVWIA 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 functional water channel protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: Homotetramer (By similarity).
SUBCELLULAR LOCATION: Integral membrane protein. Inner memb
SIMILARITY: BELONGS TO THE MIP/AQUAPORIN FAMILY (TC 1.A.8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        osmolarity.
                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
WLFWVA 209
                                                                                                                                                                                                                                                        PS00221; MIP;
                                                                                                                                                                                                                                                                   TIGR00861; MIP; 1.
                                                                                                                                                                                                                                                                                                                   IPR000425; MIP_family.
                                                                                             92
228 AA;
                                                                                                                                                                                                                                             Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Aquaporin X).
                                               Conservative
                                                                                                                                34
81
127
154
203
63
184
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149
176
225
65
186
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23145
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                                                        84.2%;
66.7%;
                                                                                              , WΜ
                                                                                                                                                                                                                                           Inner membrane;
                                             ۲,
                                                         Score 32;
Pred. No.
                                                                                                                                                                   POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                           OF THE TETRAMER (BY SIMIL POLY-ALA. 23C64C39E4DD444A CRC64;
                                                                                                                                             NPA 1.
NPA 2.
                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                 INVOLVED IN TETRAMERIZATION OR STABILITY
                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in the pathogenic bacterium
                                                        DB
88;
                                                                                                                                                                                                                                                                                                                                                                                                     There are no restrictions ong as its content is in
                                                                                                                                                                                                                                          Repeat.
                                                                                                                   (BY SIMILARITY).
                                             1;
                                                                   Length 228
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                                            Gaps
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RESULT 14

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Query Match
Best Local Similarity
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Q9L772;
15-JUN-2002
                                                                     SITE
                                                                                           TRANSMEM
REPEAT
                                                                                                                                                                                                                                                         EMBL; AF226624; AAF36396.1; -. EMBL; AE009450; AAL51252.1; -. HSSP; P29972; 1H6I.
                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         The denome security.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,
Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria;
Brucellaceae; Brucella.
                                   SEQUENCE
                                             DOMAIN
                                                                                                                                                                                                PRINTS; PR00783; MINTRINSICP. ProDom; PD000295; MIP_family; TIGRFAMS; TIGR00861; MIP; 1.
                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                  between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a
                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=16M / ATCC 23456 / Biotype 1;
MEDLINE=20020109; PubMed=11756688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning and nucleotide sequence of aquaporin melitensis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brucella melitensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aquaporin Z.
AQPZ OR BMEI0070
                                                                                                                                                                                      PROSITE; PS00221; MIP;
                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a
                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO THE MIP/AQUAPORIN FAMILY (TC 1.A.8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Suarez-Guemes F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hernandez-Castro R., Verdugo-Rodriguez A., Gutierrez-Pabello J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=29459
                                                                                 REPEAT
                                                                                                                                         FRANSMEM
                                                                                                                                                                  TRANSMEM
                                                                                                                                                                           Fransport;
                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The genome sequence of the facultative intracellular
                                                                                                                   TRANSMEM
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L5-JUN-2002
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                                                                                                                                                                                                                                     PF00230; MIP;
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228
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(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
                                   AA;
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103
149
176
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186
                                             97
                                   23189 MW;
 84.2%;
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 Score
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STRAMER (BY SIMILARITY)
 DB 1;
88;
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                                                                                                                                                                          Repeat; Complete proteome.
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          Length 228
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Search completed: January 3, 2003, 15:29:24 Job time: 6.18182 secs
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ID Y836_AQUAE
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Sest Local Similarity
Varches 4; Conserve
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TRANSMEM 4 24 POTENTIAL.
TRANSMEM 42 62 POTENTIAL.
TRANSMEM 100 120 POTENTIAL.
TRANSMEM 145 165 POTENTIAL.
TRANSMEM 145 165 POTENTIAL.
TRANSMEM 171 191 POTENTIAL.
TRANSMEM 171 191 POTENTIAL.

SEQUENCE 232 AA; 26317 MW; B934B56FEA35B183 CRC64;
                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-VF5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            067008;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical protein AQ_836.
                                                                  1 WLVWI 5
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183 WLVWL 187
                                                                                                                                                                                                                                                                                                                        EMBL; AE000709; AAC06970.1; -.
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-I- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
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NCBI_TaxID=63363;
[1]
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd

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Result
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 SPTREMBL_21:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_numan:*
5: sp_invertebrate
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_plage:*
10: sp_plant:*
11: sp_vortebrate
13: sp_vertebrate
14: sp_unclassifi
15: sp_archeap:*
16: sp_bacteriap:
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length: 2000000000
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Match Length
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 5 Q8XPT4

5 Q9K112

5 Q9CX12

6 Q967S2

6 Q8Y0V2

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6 Q9L4I1

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Q8Y8H8
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      OBYOV2 ralstonia s

QBO751 dirofilaria

QBZ9fZ salmonella

QBJGZ salmonella

Q91411 salmonella

Q9142 onchocerca

Q9673 dirofilaria

Q96753 dirofilaria
                                                                     092d92 listeria in
08y8h8 listeria mo
08y963 ralstonia s
092zh9 rhizobium m
08xpt4 ralstonia s
08xpt4 ralstonia s
08y112 anabaena sp
09ck00 pasteurella
096752 dirofilaria
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## ALIGNMENTS

Ma Be	RT REL DR DR SQ	RA RA RA RA RA	RA RA RA	OCC OCC	RESU Q92I ID AC AC
Query Match 100.0%; Score 38; DB 16; Length 371; Best Local Similarity 100.0%; Pred. No. 89; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps	Comparative genomics of Listeria species.";  CL Science 294:849-852(2001).  REMBL; AL596166; CAC96157.1;  REJILIST; LIN00925;  WHypothetical protein; Complete proteome.  SEQUENCE 371 AA; 41360 MW; 4EFE4A30E917C242 CRC64;	Gautier L., Goebel W., Gomez-Lopez N., Hain Jones LM., Kaerst U., Kreft J., Kuhn M., Madueno E., Maitournam A., Mata Vicente J., Nordsiek G., Novella S., de Pablos B., Pere. Remmel B., Rose M., Schlueter T., Simoes N. Vazquez-Boland JA., Voss H., Wehland JB.		01 DEC 2001 (ILEMBLIE). 19, Last sequence update) 01 DEC 2001 (TERMBLIE). 19, Last annotation update) 02 Putative membrane protein. 03 Risteria innocua. 04 Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales; 05 Listeria ceae; Listeria. 06 NCBI_TaxID=1642; 07 [1]	SULT 1 2D92 2D92 092D92 092D92; 01-DEC-2001 (TEMBLICAL 19, Created) 01-DEC-2001 (TEMBLICAL 19, Created)

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Best Local S
Matches 6
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A Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
A Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
A Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
A Domann E., Dominguez-Bernal G., Duchaud E., Durant C., Dussurget O.,
A Cautier L., Goebbl W., Garcia-del Portillo F., Garrido P.,
A Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
A Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
A Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
A Mordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
A Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
A Vacquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
Coience 294, 849-852(2001).
E Listifict. 12000253.
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01-MAR-2002
01-MAR-2002
          Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.;
                                                                                                                                                                                                                                           01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                   MEDLINE-21681879; PubMed-11823852;
                                                                                                                    STRAIN-GMI1000;
                                                                                                                                                                                                                      Probable inner membrane RSC1181 OR RSO5713.
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MEDLINE-21537279; PubMed-11679669;
                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                      Raistonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; beta subdivision; Raistonia group;
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Hypothetical protein; Complete proteome.
SEQUENCE 371 AA; 41252 MW; 54E7E86545CAA62E CRC64;
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Bacteria; Firmicutes; B
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plant pathogen Ralstonia solanacearum.";
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01-MAR-2002 (TrEMBLrel. 20, Created)
1 01-MAR-2002 (TrEMBLrel. 20, Last sequence
1 01-JUN-2002 (TrEMBLrel. 21, Last annotation of transmembrane TWO-component se
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                    PROSITE;
Plasmid;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-21396509; PubMed-11481432;
Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells
Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
"Nucleotide sequence and predicted functions of the entire
Sinorhizobium meliloti pSymA megaplasmid.";
Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
EMBL; AE007241; AAK65164.1; -.
         Ralstonia.
NCBI_TaxID=305
                                                Ralstonia solanacearum (Pseudomonas Plasmid megaplasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhizobium meliloti (Sinorhizobium meliloti). Plasmid pSymA (megaplasmid 1). Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae; Sinorhizobium.
                                     Bacteria;
                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001880; MSion_channel.
InterPro; IPR000504; RNA_rec_mot.
Pfam; PF00924; MS_channel; 1.
PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein RA0506 RA0506 OR SMA0937.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 415:497-502(2002).
EMBL; AL646063; CAD14883.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=382;
                                                                                                                                                                                                                                 333 WLVWVA 338
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nes 6; Conserv
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                                     Proteobacteria;
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83.3%;
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component sensor kinase
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Pred. No.
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Pred. No.
                                     subdivision;
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                                                              solanacearum).
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2.4e+02;
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                                     Ralstonia
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RESULT Q8YL12 ID YL12 QE AC QE AC QE DT 01 DT 01 DT 01 OC GN AI GN
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Best Local Similarity
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Interpro; IPR00358; Bact_sens_pr_C.
Interpro; IPR003660; HAMP.
Interpro; IPR003661; His_kina.
Interpro; IPR003659; HIS_KIN_sig.
Interpro; IPR00359; HIS_KIN_sig.
Pfam; PF00572; HAMP; 1.
Pfam; PF00572; HAMP; 1.
Pfam; PF00512; signal; 1.
Pfam; PF00512; signal; 1.
PRINTS; PR00344; BCTRLSENSOR.
SMART; SM00388; HISKA; 1.
SMART; SM00388; HISKA; 1.
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01-MAR-2002 (TrEMBLrel. 20, 1
Hypothetical protein Alr7126.
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Q8YL12;
01-MAR-2002
                                                                                                                                                                                                                                                                                    Watanabe A., Iriguchi M., Ishikawa ..., Matsuno A. Kishida Y., Kohara M., Matsumoto M., Makzawa N. Nakazaki N., Shimpo S., Sugimoto M., Takazawa N. Yasuda M., Tabata S.;
"Complete genomic sequence of the filamentous !"
                                                                                                                                                                                         cyanobacterium Anabaena sp. strain DNA Res. 8:205-213(2001).
EMBL; APO03600; BAB78210.1; -
Plasmid; Hypothetical protein; Comp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anabaena sp. (strain PCC 7120).
Plasmid pCC7120alpha.
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc
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EMBL; AL646085; CAD18704.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21595285; PubMed=11759840;
Kaneko T., Nakamura Y., Wolk C.P.,
Watanabe A., Iriguchi M., Ishikawa
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MEDLINE=21681879; PubMed=11823852;
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369 WLVWLA
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A28879BB7E0B074D CRC64;
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A., Kawashima
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ima K., Kimura T.,
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Muraki A.,
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RESULT

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Q967S2;
Q1-DEC-2001
Q1-DEC-2001
Q1-JUN-2002
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Q9CK00;
01-JUN-2001
01-JUN-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                 Crossgrive K., Laudet V., Maina C.V.;

"Dirofilaria immitis encodes dinhr-7, a putative homolog

Drosophila ecdysone-regulated E78 gene.";

Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.

-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS

EMBL; AP367207; AARS4128.1;

InterPro: IPR000536; Hormone_rec_lig.

InterPro: IPR001628; Znf_C4steroid.
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                                                                                                                                                                            Zinc-finger.
SEQUENCE
                                                                                                                                                                                                                                                       Pfam; PF00104; hormone_rec; Pfam; PF00105; zf-C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dirofilaria immitis
Eukaryota; Metazoa;
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166 WLVWIS 171
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                      1 WLVWIA 6
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. (TrEMBLrel. 17, 1
. (TrEMBLrel. 19, 1
. protein PM1838.
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                                                                                       Conservative
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83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             heartworm).
a; Chromadorea;
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                                                                                                         Score 35; DB 5;
Pred. No. 2.6e+02;
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0B31A94DD2AAA2F9 CRC64;
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. 1.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spirurida;
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                                                                                                                           Length 358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 234;
                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 T.S.; K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Filarioidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               of
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                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               the
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                                                                                    Gaps
                                                                                    0;
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Chandler M., Billault A., Brottler P., Camus J.C., Cattolico L.,
Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N.,
Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RT Nature 415:497-502(2002).
DR RHBL; AL646061; CAD14643.1; -
DR InterPro: IPR001915; Peptidase_M48.
DR Pfam; PF01445; Peptidase_M48; 1.
KW Hydrolase; Complete proteome.
SQ SEQUENCE 418 AA; 46610 MW; BACCDD9903CBERE? ^---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SQ DR RA
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Q8Y0V2
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001638; Znf_C4steroid.
Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
ProDom; PD000035; Znf_C4steroid; 1.
PROSITE; PS000031; NUCLEAR_RECEPTOR; UNKNOWN_1.
   SEQUENCE
                                                                                                      Q967S1;
01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08Y0V2;
01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                Q967S1
                      DNA-binding; Nuclear protein;
                                                                                                                                                                                                                        Eukaryota; Metazoa; Nematoo
Onchocercidae; Dirofilaria
                                                                                                                                                                                                                                                                       Nuclear receptor nhr-7C
                                                                                                                                                                                                                                                Dirofilaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-GMI1000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; beta subdivision; Ralsto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8Y0V2
            Zinc-finger
                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                             NCBI_TaxID=6287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=305;
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                                                                                                                                                                                                                                                                                                                                                                                                             1 WLVWIA 6
   463
                                                                                                                                                                                                                                   immitis (Canine heartworm).
Metazoa; Nematoda; Chromadorea;
                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
  AA;
  52253 MW;
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83.3%;
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19,
21,
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                               PRT;
                        Receptor;
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  A3430D0FAC35DF8E CRC64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                No. 2
                                                                                                                                                                                                                                                                                                                               463 AA
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                        Transcription regulation,
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les 0;
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                                                                                                                                                                                                                                   Spirurida; Filarioidea;
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RESULT 12
Q9L4I1
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Q8Z9F2
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Best Local S
Matches 5
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Best Local S
Matches 5
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Q8Z9F2;
01-MAR-2002 (TrEMBLrel. 2
01-MAR-2002 (TrEMBLrel. 2
01-JUN-2002 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T. T., Hollroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J. Starry C., Whitehear's "
  Cano D., Casadesus J., "Characterization of a
                                           STRAIN-SL1344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001092; HLH_basic.
InterPro; IPR001092; Na/Gal_symp.
InterPro; IPR001927; Na/Gal_symp.
TIGREAMS; TIGR00792; gph; 1.
PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
Hypothetical protein; Complete proteome.
Hypothetical protein; Complete proteome.
SEQUENCE 468 AA; 52589 MW; 883F0D9F7F8D3A87 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genome sequence of a enterica serovar Typhi CT18.";
Nature 413:848-852(2001)
EMBL: AL627265; CAD01308.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Parkhill J., Dougan G., James K.D.,
Churcher C., Mungall K.L., Bentley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Putative symporter STY0171.
                                                                  SEQUENCE FROM N.A.
                                                                                                         NCBI_TaxID=602;
                                                                                                                                     Salmonella
                                                                                                                                                                              Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21534947; PubMed=11677608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-CT18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=601;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella typhi
                                                                                                                                                     Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Whitehead
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                                                                                                                                                                                typhimurium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92.1%;
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83.3%;
Garcia-del Portillo
Salmonella-specific
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20,
                                                                                                                                                       gamma subdivision; Enterobacteriaceae;
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Pred.
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Pred.
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No.
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0;
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F.; region located between
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RESULT 14
Q9U6X2
ID Q9U6X
AC Q9U6X
DT 01-MP
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Q19337
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Best Local S
Matches 5
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Q9U6X2
Q9U6X2;
01-MAY-2000
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Q19337;
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EMBL; AE008700; AAL19113.1; -.
InterPro; IPR001092; HLH_basic.
InterPro; IPR001927; Na/Gal_symp.
TIGRFAMs; TIGR00792; gph; 1.
PROSITE; PS00038; HELY_LOOP_HELIX; UNKNOWN_1.
Hypothetical protein; Complete proteome.
Hypothetical protein; S2443 MW; 5545B43CB3EA0B3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-LT2 / SGSCi412 / ATCC 700720;

MEDLINE-21534948; PubMed-11677609;

McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                           investigating biology ";
Science 282:2012-2018(1998).
EMBL; 268297; CAA92595-1; -.
SEQUENCE 536 AA; 60611 MW;
                                                                                                                                                                                                                                       none;
                                                                                                                                                                                                                                                  MEDLINE=99069613;
                                                                                                                                                                                                                                                                                      Submitted
                                                                                                                                                                                                                                                                                                  Smye
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans
Eukaryota; Metazoa; Ner
                                                                                                                                                                                                                                                                                                                                                                                 F11A10.5
                                                                                                                                                                                                                                                                                                                                                                                        F11A10.5 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete genome sequence of Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and aroP genes.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                               Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
                                                                                                                                                                                                                           "Genome sequence of the nematode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13
                                                                                                                               Local Similarity
les 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82 WLLWIA 87
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                                                                                  WLLWIA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
5; Conser
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 (TrEMBLrel. 13,
                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                             N.A.
                                                                                                                                                                                                                                                  PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                         Nematoda; Chromadorea;
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83.3%;
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83.3%;
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Pred. No. 3.3e
1; Mismatches
                                                                                                                              Score 35; DB Pred. No. 3.76
1; Mismatches
                        PRT;
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                                                                                                                                                    Length 536;
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RESULT
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01-DEC-2001 (TREMBLEEL 19,

01-DEC-2001 (TREMBLEEL 19,

01-JUN-2002 (TREMBLEEL 21,

01-JUN-2002 (TREMBLEEL 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local
                                                                                                      Drosophila ecdysone-regulated E78 gene.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-:- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY)
-:- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS
EMBL; AF367206; AAK54127.1;
                                                                                                                                                                                                              Onchocercidae; I
NCBI_TaxID=6287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nuclear hormone receptor.
Onchocerca volvulus.
Eukaryota; Metazoa; Nematoda;
                                 ProDom; PD000035; Znf_C4steroid; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; UNKNOWN_1
                                                       Pfam; PF00104; hormone_rec; Pfam; PF00105; zf-C4; 1.
                                                                                                                                                                 Crossgrove K., Laudet V., Maina C.V., "Dirofilaria immitis encodes dinhr-7,
                                                                                                                                                                                                                                        Eukaryota;
                                                                                                                                                                                                                                                    Dirofilaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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SMART; SM00399; ZnF_C4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00398; STRDHORMONER.
PRINTS; PR00047; STROIDFINGER.
PRODOM; PD000035; Znf_C4steroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00104; hormone_rec; 1. Pfam; PF00105; zf-C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- SUBCELLULAR LOCATION: NUCLEAR (BY S-i- SIMILARITY: BELONGS TO THE NUCLEAR EMBL; AF170551; AAF06997.1; -.
HSSP; P20393; 1A6Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            wolvulus."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE=20058753; PubMed=10593180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Onchocercidae; Onchocerca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2002 (TrEMBLrel. 21,
                                                                               InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001628; Znf_C4steroid.
                                                                                                                                                                                                                                                                NHR-7
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         Zinc-finger
                     DNA-binding; Nuclear protein;
                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
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nes 5; Conserv
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IPR001723; Stdhrmn_receptor.
IPR001628; Znf_C4steroid.
556
                                                                                                                                                                                                                                        Metazoa;
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AA;
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63342
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83.3%;
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MW;
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Pred. No.
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                      Receptor;
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2F7995FAFEB5126F CRC64;
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                      Transcription regulation;
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                                                                                                                    RECEPTORS
                                                                                                                                                                 homolog
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from Onchocerca
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Query Match
92.1%; Score 35; DB 5; Length 556;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 WLVWIA 6
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Db 364 WLVWIS 369

Search completed: January 3, 2003, 15:32:04
Job time : 21.3182 secs
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Result
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
80
                                                                                                                                                                                                                                                                                        Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq length: 0
seq length: 2000000000
    Issued_Patents_AA:*
1: /cgn2_6/ptodata/1
2: /cgn2_6/ptodata/1
3: /cgn2_6/ptodata/1
4: /cgn2_6/ptodata/1
5: /cgn2_6/ptodata/1
6: /cgn2_6/ptodata/1
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38
1 WLVWIA 6
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   262574 seqs,
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                                                                                                                                                                                                                                                                                                                                                                              /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/BCTUS_COMB.pep:*
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US-08-4469-260A-478
US-08-137-1170-35
US-08-436-717-35
5234657-5
5244657-5
5433945-5
US-09-112-126B-2
US-09-116-080-5
US-09-316-080-2
US-09-316-080-2
US-09-316-080-2
US-08-63-566A-15
US-08-63-566A-15
US-08-63-566A-15
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US-08-63-566A-15
US-08-63-566A-15
US-08-63-566A-15
US-08-36-240A-15
PCT-US95-10245-15
US-08-36-240A-15
PCT-US95-1045-15
US-08-36-240A-15
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PCT-US93-08528-16
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(without alignments)
19.615 Million cell updates/sec
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Compugen Ltd
Sequence 478, App
Sequence 35, Appl
Sequence 35, Appli
Patent No. 5223610
Patent No. 5234657
Patent No. 543945
Sequence 5, Appli
Sequence 5, Appli
Sequence 2, Appli
Sequence 19, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 15, Appl
Sequence 2, Appli
                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                                                                               Patent No.
                                                                                                                                                                                                                                              16, Appl
16, Appl
5. 5200183
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1 WLVWI 5

Query Match
Best Local Similarity
Matches 4; Conserv

Conservative

1,

86.8%; 80.0%;

Score 33; DB 1; Le Pred. No. 3.7e+02; "" cmatches 0;

Length 362; Indels

0

Gaps

RESULT 1  US-08-118-270-16  US-08-118-270-16  Sequence 16, Appl  Patent No. 550838  GRMERAL INFORMAT  APPLICANT: MU  APPLICANT: MU  APPLICANT: MU  APPLICANT: SEC  TITLE OF INVEN  TITLE OF INVEN  USTREET: 419  COUNTRY: Washi  STATE: D.C.  COUNTRY: Washi  STATE: D.C.  COUNTRY: Washi  STATE: D.C.  COUNTRY: Washi  STATE: APPLICATION  FILING DATE:  COMPUTER READA  MEDIUM TYPE:  COMPUTER: I.  OPERATION  FILING DATE:  PRIOR APPLICATION  FILING DATE:  PRIOR APPLICATION  FILING DATE:  ATTORNEY AGENT  NAME: TOWNS  REGISTRATION  REFERENCE/DO  TELEFONMUNICAT  TELEPHONE:  TELEPHONE:  TELEPT 2486  INFORMATION FOR SEQUENCE CHARM  LENGTH: 362  TYPE: amino  STRANDEDMESS  TOPOLOGY: 1  MOLECULE TYPE:  WALE: TYPE:  MOLECULE TYPE:	28 29 30 31 32 33 33 33 30 30 30 30 30 30 30 30 30 30
Application Application Application 508384 S08384 S08384 S0838 SCHENTION: SCHUSTER; INVENTION: INVENTION: INVENTION: INVENTION: SCOURCES EE: BROWDY 419 Sevent Washington D.C. INVENTION IN OUA BREADABLE FOR READABLE FOR STIDN NUMBER: INFORM DOWNERS INFORM AND INFORM DOWNERS IN 202-628 IN 202-638 FOR SEO ID JHARACTERISOT 362 amino acid MNESS: Sing YPPE: pepti 166	78.9 24 4 78.9 24 4 78.9 52 4 78.9 52 2 78.9 52 2 78.9 52 2 78.9 52 2 78.9 52 3 78.9 52 3 78.9 143 3 78.9 143 3 78.9 143 4 55 55 56 56 56 56 56 56 56 56 56 56 56 5
B. I. B. I. B. I. B. I. B. I. B. I. CORS, AND COMPOSITION SIMARK SET, N.W., Suite 300 SIMARK SET, N.W., Suite 300 SIMARK SET, N.W., Suite 300 BLIE SIMS-DOS SIMS-	US-08-776-949-2 US-08-482-8110-2 US-09-036-805-2 US-09-258-128-2 US-08-470-419-4 US-08-761-828-4 US-08-76-949-4 US-08-76-949-4 US-08-482-8110-4 US-09-636-805-4 US-09-636-805-4 US-09-636-805-4 US-09-363-526-11 US-09-363-526-11 PCT-US94-01149-69
S AND METHODS THEREOF	Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 1, Appli Sequence 11, Appli

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120 WLVWV 124

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RESULY 4

PCT-US93-08528-16
; Sequence 16, Application PC/TUS9308528
; GENERAL INFORMATION:
; APPLICANT: New York University
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
   ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                         RESULT 3
5200183-5
5200183-5
                                APPLICATION NUMBER: 504,635
FILING DATE: 04-APR-1990
APPLICATION NUMBER: 122,410
FILING DATE: 19-NOV-1987
SEQ ID NO:5:
                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: 11;
; MOLECULE TYPE:
PCT-US93-08528-16
                                                                                                                                                                                                                                                                       Patent No. 5200183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO:
                                                                                                                              APPLICATION NUMBER: US/
FILING DATE: 12-JUN-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                       APPLICANT: TANG, JORDAN J.N.; WAN
TITLE OF INVENTION: RECOMBINANT
NUMBER OF SEQUENCES: 22
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 362 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                     120 WLVWV 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                  LENGTH: 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY-2 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: UZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 80.0 es 4; Conservative
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                                                                                                                                                                                                                               JORDAN J.N.; WANG, CHI-SUN
ON: RECOMBINANT BILE SALT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                86.8%;
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1; Mismatches
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J. 3.7e+02;
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RESULT 5 US-08-137-117D-35

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Вb
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US-08-469-260A-478
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Best Local Similarity 80.4
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                     TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: POREWBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: I
FILING DATE:
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ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ANYHONY SCOTT MUERHOFF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUIDK
APPLICANT: ISA K. MUSHAHWAR
TITLE OF INVENTION: NON-A, NON-B. NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                    TELEPHONE: 706 - 708-938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/469,260A FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 60064-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 100 ABBOT'
CITY: ABBOTT PARK
STATE: IL
| | | |:|
2 WLTWLA
                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
                                                                                 Local Similarity
                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 WLVWI 5
                                 1 WLVWIA 6
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TAMI J. PILOT-MATIAS
GEORGE J. DAWSON
GEORGE G. SCHLAUDER
SURESH M. DESAI
THOMAS P. LEARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 ABBOTT PARK ROAD
                                                                                                                                                                                                 75 amino acids
                                                                   Conservative
                                                                                 84.2%;
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                                                                                 Score 32; DB 4;
Pred. No. 1.2e+0;
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Pred. No. 5.8e+02;
                                                                                 .2e+02;
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US-08-436-717-35
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                                                                                                                                    Sequence 35, Application US/08436717 Patent No. 5817790
                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 5346
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEFAX: 904136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, JOSE
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 20-DEC-199
                                                                                  APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: JP 3-95476 FILING DATE: 25-APR-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: JP 4-FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: WO PO
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR NUMBER OF SEQUENCES: 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 3000 K STREET: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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3000 K Street, N.W., Suite 500
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JONES, Steven
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                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          linear
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20-DEC-1993
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80.0%;
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                                                                                                                                                                                                                                                                                                                    Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                        Mismatches
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RESULT 7
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                                                                                                        5223610-5
                                                                                                                                                                                                                                                         ; Patent No. 5223610
                                                                                                                                                                                                             APPLICANT: Burton, Frank H.;Sutcliffe, Gregor
TITLE OF INVENTION: CHOLERA TOXIN GENE REGULATED
HORMONE PROMOTER
                                                                                                                                      SEQ ID NO:5:
                                             Matches
                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (202)672-539
TELEX: 904136
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-9
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,25
                                                                                                                                                                 NUMBER OF SEQUENCES: 18
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US/08/137,117
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
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                                                       Local Similarity
                                                                                                                                    FILING DATE: 18-MAY-1990
) NO:5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE:
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                                                                                                                      LENGTH: 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
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1 WLVWIA 6
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20007-5109
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                                             Conservative
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80.0%;
                                                            84.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53466/126/AAOK
                                            Score 32; DB 6;
Pred. No. 3.9e+02;
1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                              Score 32; DB 2;
Pred. No. 2.1e+02;
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                                                                        Length 266;
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                                             Indels
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15 WLTWLA

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Sequence 2, Application US/09122126B

Patent No. 6451575

GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
FILE REFERENCE: DM6909

CURRENT APPLICATION NUMBER: US/09/122,126B

CURRENT FILING DATE: 1998-07-24

NUMBER OF SEQ ID NOS: 21

SOFTWARE: PatentIn version 3.0

SEQ ID NO 2

LENGTH: 837
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5433945-5
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US-09-122-126B-2
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NUMBER OF SEQUENCES: 10
CURRENT APPLICATION DATA:
CURRENT APPLICATION UNMBER: US/07/979,798
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; APPLICANT: KLEIN, MICHEL H.;BOUX, HEATHER A.;COCKLE,
;STEPHEN A.;LOOSMORE, SHEENA M.;EEALEY, GAVIN R.
TITLE OF INVENTION: IMMUNOPROTECTIVE GENETICALLY-DETOXIFIED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;Patent No. 5244657
; APPLICANT: KLIEN, MICHEL A.;BOUX, HEATHER A.;COCKLE,
;STEPHEN A.;LOOSMORE, SHEENA M.;ZEALEY, GAVIN R.
; TITLE OF INVENTION: GENETIC DETOXIFICATION OF PERTUSSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOXIN
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Best Local Similarity

Matches 4; Conserv
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Best Local Similarity
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FILING DATE: 20-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 589,423
FILING DATE: 28-SEP-1990
APPLICATION NUMBER: 275,376
FILING DATE: 23-NOV-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/589,423
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 275,376
FILING DATE: 23-NOV-1988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 269
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Pred. No. 3.9e+02;
1; Mismatches 1
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Pred. No. 3.9e+02;
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US-08-469-260A-534
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                                            Query Match
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                                                                                                                                                                                   TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: JOHN N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: SURESH M. DESAI

APPLICANT: THOMAS P. LEARY

APPLICANT: ANTHONY SCOTT MUERHOFF

APPLICANT: JAMES C. ERKER

APPLICANT: SHERI L. BUIJK

APPLICANT: SHERI L. BUIJK

APPLICANT: ISA K. MUSHAHWAR

TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS

TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE

NUMBER OF SEQUENCES: 716
                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: POREMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527
                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES
STREET: 100 ABBOTT PARK ROAD
                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 708-937-6365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                            TELEPHONE: 708 -2623
                                 Local Similarity
nes 3; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 WLVWL 37
                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/469,260A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
                                                                                                                                                           LENGTH:
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GEORGE G. SCHLAUDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAMI J. PILOT-MATIAS
                                 Conservative
                                                                                                            protein
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                                               81.6%;
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                                               Score 31;
Pred. No.
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Pred. No. 1.2e+03;
                                 Mismatches
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                                              DB 4; I
1.1e+02;
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LENGTH: 380
TYPE: PRT
ORGANISM: Fusarium
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; LENGTH: 377
; TYPE: PRT
; ORGANISM: Fusarium
                                                                           Query Match
Best Local S
Matches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: John C. Royer
APPLICANT: Lynne M. Christianson
APPLICANT: Gregory A. Gambetta
APPLICANT: Howard Brody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: John C. Royer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence 2, Application US/09316080 Patent No. 6180366
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Best Local S
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                                                                                                                                                                                                                                                                                                APPLICANT: Suzanne M. Otani
APPLICANT: Wendy T. Yoder
ITILE OF INVENTION: Methods For Producing Heterologous
TITLE OF INVENTION: Methods For Producing Heterologous
TITLE OF INVENTION: Molypeptides In Trichothecene-Deficient Filamentous Fungal
TITLE OF INVENTION: Mutant cells
TITLE REFERENCE: 5563.200-US
CURRENT APPLICATION NUMBER: US/09/316,080
CURRENT FILING DATE: 1999-05-20
EARLIER APPLICATION NUMBER: 09/082,217
EARLIER FILING DATE: 1998-05-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Suzanne M. Otani
APPLICANT: Wendy T. Yoder
ITTLE OF INVENTION: Methods For Producing Heterologous
ITTLE OF INVENTION: Methods For Producing Heterologous
ITTLE OF INVENTION: Mutant Cells
FILE FILE OF INVENTION: Mutant Cells
FILE REFERENCE: 5563.200-US
CURRENT APPLICATION NUMBER: US/09/316,080
CURRENT FILING DATE: 1999-05-20
EARLIER FILING DATE: 1999-05-20
ARLIER FILING DATE: 1999-05-20
UMMBER OF SEQ ID NOS: 24

NUMBER OF SEQ ID NOS: 24

SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Gregory A. Gambetta
APPLICANT: Howard Brody
                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 3.0
220 WMVWV 224
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nes 3; Conserv
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                                     1 WLVWI 5
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                                                                                              81.6%;
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                                                                                              Score 31; DB 4;
Pred. No. 7.6e+02;
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Pred. No. 7.5e+02;
                                                                             Mismatches
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RESULT 15
US-08-663-566A-19
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Best Local Similarity
Thes 3; Conserve
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                                                                                                                                                                                                                                                                                                            Sequence 19, Application US/08663566A Patent No. 5853733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence 2, Application US/08952365
Patent No. 6274311
                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Cochran, Mark D
APPLICANT: Macdonald, Richard D
TITLE OF INVENTION: Recombinant
TITLE OF INVENTION: and Uses The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 438 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda m.
REGISTRATION NUMBER: 34,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTYWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                             133 WMVWV 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: Canada
ZIP: M5H 3Y2
                                                                                               COUNTRY: US
ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Toronto
STATE: Ontario
                                                                                                                                             CITY: New York
                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE:
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                                                                                                                                 New York
                                                                                                                                                            1185 Avenue of the Americas
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                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (416)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (416) 364-7311
(416) 361-1398
R SEQ ID NO: 2:
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                                                                                                                                                                                                                             and Uses
                                                                                                                                                                                                                                          Recombinant Herpesvirus
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Pred. No. 8.70
2; Mismatches
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                 Version #1.25
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J.7e+02;
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APPLICATION NUMBER: US/08/663,566A

FILING DATE: June 13, 1996

CLASSIFICATION: 415

ATTORNEY/AGENT INFORMATION:
NAME: White, John P

REGISTRATION NUMBER: 28,678

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)278-0400
TELEFAX: (212)391-0526
TELEX: 42253

INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 705 amino acids
TYPE: amino acids
TYPE: minion acids
TYPE: protein
HYPOTHETICAL: NO
US-08-663-566A-19

Nuery Match
ANTI-SENSE: NO
US-08-663-566A-19

Nest Local Similarity 66.7%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 1; Indels
Oy 1 MILVWIA 6

OY 1 MILVWIA 645

Search completed: January 3, 2003, 15:34:32

Search completed: January 3, 2003, 15:34:32
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
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         117078 seqs, 18951520 residues
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Gapop 10.0 , Gapext 0.5
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38
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                                                                                                                                                                                                                                                                                                                                      Published_Applications_AA: *
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Listing first 45 summaries
:/cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
:/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
:/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
:/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
:/cgn2_6/ptodata/1/pubpaa/US07_NEW_MPUB.pep:*
:/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
:/cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
:/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
:/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
:/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
:/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
:/cgn2_6/ptodata/1/pubpaa/US00_NEW_PUB.pep:*
:/cgn2_6/ptodata/1/pubpaa/US00_NEW_PUB.pep:*
:/cgn2_6/ptodata/1/pubpaa/US00_NEW_PUB.pep:*
:/cgn2_6/ptodata/1/pubpaa/US00_NEW_PUB.pep:*
:/cgn2_6/ptodata/1/pubpaa/US00_NEW_PUB.pep:*
:/cgn2_6/ptodata/1/pubpaa/US00_NEW_PUB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2003, 15:32:11; Search time 4.77273 Seconds (without alignments)
23.825 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117078
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Score	Query Match	Query Match Length	DB	ID	Description
1	37	97.4	230	9 :	US-09-738-626-3571	Sequence 3571, Ap
2	34	89.5	49	10	US-09-995-494-75	e 75, i
ω	34	89.5	420	10	US-09-815-242-11260	3
4	33	86.8	296	10	US-09-741-669-378	Sequence 378, App
ъ	33	86.8	735	10	US-09-815-242-12089	12089
O	32	84.2	75	æ	US-08-424-550B-478	Sequence 478, App
7	32		110	10	US-09-867-550-298	Sequence 298, App
8	32	84.2	560	10	US-09-815-242-11746	11746
9	32	84.2	837	12	US-10-052-586-352	Sequence 352, App
10	31	81.6	50	8	US-08-424-550B-534	Sequence 534, App
11	31	81.6	73	10	US-09-864-761-37732	Sequence 37732, A
12	31	81.6	86	10	US-09-864-761-48030	Sequence 48030, A
13	31	81.6	96	10	US-09-864-761-33793	Sequence 33793, A
14	31	81.6	126	10	US-09-864-761-48848	
15	31	81.6	401	10	US-09-871-874-11	Sequence 11, Appl
16	31	81.6	438	10	US-09-894-993-2	Sequence 2, Appli
17	31	81.6	441	10	US-09-871-874-21	Sequence 21, Appl
18	31	81.6	441	10	US-09-895-686-1	Sequence 1, Appli
19	31	81.6	445	9	US-09-992-598-177	177

	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
	31	31	31	31	31	<u>3</u> 1	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	<u>ω</u>	<u>კ</u>	31	31
	81.6		81.6			٠			•	٠		•	81.6	٠	81.6		1.	۲.	۳.	۲.	1.		۳.	۳	81.6	<u>,                                    </u>
	451	446	446	446	445	445	445	445	445	445	445	445	445	445	445	445	445	445	445	445	445	445	445	445	445	445
	10	10	10	9	12	12	10	10	10	10	10	10	10	10	10	10	10	10	9	9	9	9	9	9	9	9
	US-09-871-874-9	US-09-951-780-2	US-09-871-874-10	US-09-738-626-6356	US-10-052-586-148	US-10-006-867-32	US-09-989-721-177	US-09-990-456-177	US-09-993-604-177	US-09-991-163-177	US-09-990-442-177	US-09-991-073-177	US-09-989-732-177	US-09-989-731-177	US-09-989-727-177	US-09-989-279-177	US-09-989-723-177	US-09-989-722-177	US-09-993-687-177	US-09-991-181-177	US-09-990-436-177	US-09-989-730-177	US-09-990-444-177	US-09-989-735-177	US-10-063-547-32	US-09-989-293A-177
•	Sequence 9, Appli	Sequence 2, Appli	Sequence 10, Appl	Sequence 6356, Ap	Sequence 148, App	Sequence 32, Appl	Sequence 177, App	177	Sequence 177, App	Sequence 177, App	177	Sequence 177, App	Sequence 177, App	Sequence 177, App	177	Sequence 177, App	Sequence 177, App	Sequence 177, App		177			Sequence 177, App		Sequence 32, Appl	Sequence 177, App

ALIGNMENTS

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RESULT 1
US-09-738-626-3571
Sequence 3571, Application US/09738626
Publication No. US20020197605al
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: HAVASHI, MIKIRO
APPLICANT: HAVASHI, MIKIRO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: UKEDA, MASATO
APPLICANT: OCAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 199-12-16
PRIOR APPLICATION NUMBER: JP 90/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SEQ ID NO 3571
LENGTH: 230
TYPE: PRT
CORANISM: Corynebacterium glutamicum
US-09-738-626-3571
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; ORGANISM: Homo sapien
US-09-995-494-75
            SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 11260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. US20020061569A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes FILE REFERENCE: DEX-0293
CURRENT APPLICATION NUMBER: US/09/995,494
CURRENT FILING DATE: 2001-11-27
PRIOR APPLICATION NUMBER: 60/253,176
PRIOR FILING DATE: 2000-11-27
NUMBER OF SEQ ID NOS: 115
SOUTWARE: PATENTIN Version 3.1
SEQ ID NO 75
LENGTH: 49
TWO TO THE PRIOR OF SEQ ID NOS: 115
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                                                                    PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                          FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Xu, H. Howard further of INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
                                                        NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
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APPLICANT: Macina, Roberto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Haselbeck, Robert
ENGTH:
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                                                                                                                            APPLICATION NUMBER: 60/242,578
FILING DATE: 2000-10-23
APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
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Liu, Chenghua
Chen, Sei-Yu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cafferkey, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carr, Grant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ali, Shujath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamamoto, Robert T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recipon, Herve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/09815242
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RESULT 4
US-09-741-669-378
; Sequence 378, Application
; Patent No. US20020022718A1
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Best Local Similarity
Matches 5; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Escherichia coli
US-09-741-669-378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Haemophilus influenzae US-09-815-242-11260
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 481
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 378
LENGTH: 296
TYPE: PRT
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12089, Application US/09815242 Patent No. US20020061569A1
                                                                                                                   TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERNCE: ELITER. 011A,
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-815-242-12089
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Genes identified as required for TITLE OF INVENTION: proliferation of E. coli FILE REFERENCE: ELITRA.009A
                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Forsyth, R. Allyn
Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                                                                                                                Carr, Grant J.
Yamamoto, Robert T
Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                   Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                    Trawick, John D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34;
Pred. No.
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95;
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; TOPOLOGY: 1i
; MOLECULE TYPE:
US-08-424-550B-478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT ; ORGANISM: Pseudomonas aeruginosa US-09-815-242-12089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-424-550B-478
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FRSTSEQ for Windows Version 4.0
SEQ ID NO 12089
LENGTH: 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 478, Application US/08424550B Patent No. US20020119447A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 86.8%;
Best Local Similarity 80.0%;
Matches 4; Conservative
                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: JOHN N
                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: POREMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: TAMI J. PILOT-MATIAS
APPLICANT: GEORGE J. DAWSON
APPLICANT: GEORGE G. SCHLAUDER
APPLICANT: SURESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: JAMES C. EKKER
APPLICANT: JAMES C. EKKER
APPLICANT: SHERI L. BUIJK
APPLICANT: SHERI L. BUIJK
APPLICANT: INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 7.16
                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 75 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES
STREET: 100 ABBOTT PARK ROAD
                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          469 WLIWI 473
                                                                                                                                                                                  TELEPHONE: 706-938-2623
                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435435
                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                   84.2%;
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                   Score 32;
Pred. No.
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Pred. No. 2.3e+02;
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ed. No. 39;
Mismatches
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                                    DB 8;
                                  Length 75;
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CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191.078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
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LENGTH: 110
TYPE: PRT
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APPLICANT:
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TITLE OF INVENTION: No. US20020082206Alel Polynucleotides
TITLE OF INVENTION: Thereby
FILE REFERENCE: 21402-013 (Cura-313)
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 2001-09-20
CURRENT FILING DATE: 2001-09-20
                                                                                                                                                                                                                                                                                        APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yanamotto, Robert T.
APPLICANT: Yanamotto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: USSN 60/208,427
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 2125
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APPLICANT: Mehraban, Fuad,
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FEATURE:
NAME/KEY: VARIANT
LOCATION: (37)
COTHER INFORMATION: wherein Xaa may be any one of Ser or Pro or Thr or
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Conley, Pamela
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Pred. No. 55;
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FRSEXEQ for Windows Version 4.0
SEQ ID NO 11746
LENGTH: 560
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-815-242-11746
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Patent No. US20020127584A1
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PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/059266 PRIOR FILING DATE: 1997-09-18
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 APPLICATION
                   FILING DATE:
                                                               FILING DATE: 1997-11-13
APPLICATION NUMBER: 60/066120
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FILING DATE: 1997-10-28
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FILING DATE: 1997-10-21
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FILING DATE: 1997-10-24
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FILING DATE: 1997-10-29
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FILING DATE: 1997-10-24
                                 APPLICATION NUMBER: 60/066466
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APPLICATION NUMBER:
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FILING DATE: 1997-10-31
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Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wood, William I.
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NUMBER: 60/066772
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FILING DATE: 1998-04-20
APPLICATION NUMBER: 60/083559
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APPLICATION NUMBER: 60/085579
FILING DATE: 1998-05-15
                                                                               APPLICATION NUMBER: 60/084643 FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/085573
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APPLICATION NUMBER: 60/082569
FILING DATE: 1998-04-21
APPLICATION NUMBER: 60/082704
FILING DATE: 1998-04-22
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APPLICATION NUMBER: 60/081070
FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081195
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APPLICATION NUMBER: 60/084639
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APPLICATION NUMBER: 60/068017
FILING DATE: 1997-12-18
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APPLICATION NUMBER: 60/069425
FILING DATE: 1997-12-12
APPLICATION NUMBER: 60/069870
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NUMBER: 60/
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60/080194 60/080107 60/079786 60/079664 60/078886

60/077632 60/077450 60/069335

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APPLICATION NUMBER:

60/085582

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FILING DATE: 1998-06-04
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FILING DATE: 1998-06-16
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FILING DATE: 1998-06-09
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RESULT 11
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                    ZIF: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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                                                                                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: pro
                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
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APPLICANT: SHERI L. BUJJK
APPLICANT: ISA K. MUSHAHWAR
TITLE OF INVENTION: NON-A, NON-B. NON-C, NON-D, NON-E |
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
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708-938-2623
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                                                                                                                                                                                                                                                                                                                                    NAME: POREMBSKI, PRESISTRATION NUMBER:
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TAMI J. PILOT-MATIAS
GEORGE J. DAWSON
GEORGE G. SCHLAUDER
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Pred. No.
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US-09-864-761-37732
                            Query Match
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          Matches
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SOFTWARE: Annomax Sequence Lis
TO ID NO 37732
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00665
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00667
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       Conservative
                                                                                                                 N: EXPRESSED IN HBL100, SIGNAL = 0.99

N: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2

N: EXPRESSED IN LUNG, SIGNAL = 1.3

N: EXPRESSED IN BONE MARROW, SIGNAL = 1.2

N: EXPRESSED IN HEAR, SIGNAL = 1.1

N: EXPRESSED IN HEART, SIGNAL = 1.1

N: EXPRESSED IN PLACENTA, SIGNAL = 1.3

N: EXPRESSED IN BT474, SIGNAL = 1.3

N: EXPRESSED IN BT474, SIGNAL = 1.5

N: EXPRESSED IN BARIN, SIGNAL = 1.5

N: EXPRESSED IN BARIN, SIGNAL = 1.2

N: EXPRESSED IN BARIN SIGNAL = 1.2
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ESSED IN HBL100, SIGNAL IN FETAL LIVER, SIGNAL IN FORMER SIGNAL IN TOOM, 5
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US 09/608,408
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  Score 31; DB Pred. No. 54; 1; Mismatches
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US-09-864-761-48030
; Sequence 48030, Application
; Sequence US20020048763A1
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LENGTH: 86
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Best Local
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SOFTWARE: Annomax Sequence
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PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
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PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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PRIOR APPLICATION NUMBER: GB 24263.6
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PRIOR APPLICATION NUMBER: US 09/632,366
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                      Local
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
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APPLICATION NUMBER: US 60/234,687
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APPLICATION NUMBER: PCT/US01/00664
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T: Chen, Wensheng
T: Chen, Wensheng
INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
NINVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
  Similarity 4; Conserv
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EXPRESSED IN LUNG, SIGNAL = 1.2
EXPRESSED IN HELA, SIGNAL = 1.4
EST_HUMAN HIT: BE398071.1, EVALUE 2.00e-03
SWISSPROT HIT: P05882, EVALUE 5.20e-01
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NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence
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CURRENT FILING DATE: 2001-05-23
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                                                    OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                       OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                         OTHER INFORMATION: OTHER INFORMATION:
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OTHER INFORMATION: MAP
                                                                                                                                                                                                                                  LENGTH: 96
TYPE: PRT
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APPLICATION NUMBER: US 60/236,359
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APPLICATION NUMBER: US 09/608,408
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                                      INFORMATION:
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                     INFORMATION:
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Chen, Wensheng
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SED IN BT474,
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                              N HEART, SIGNAL = 2.3
IN HEART, SIGNAL = 1.
IN HELA, SIGNAL = 2.9
IN LUNG, SIGNAL = 1.6
IN FETAL LIVER, SIGNAL = 1.
IN PLACENTA, SIGNAL = 1.2
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US-09-864-761-33793
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                                                                                             SOFTWARE: Announce
SEQ ID NO 48848
FENGTH: 126
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
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PRIOR APPLICATION NUMBER: PCT/US01/00667
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PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
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PRIOR APPLICATION NUMBER: US 60/236,359
FEATURE:
OTHER INFORMATION: MAP TO AC010368.2
OTHER INFORMATION: EXPRESSED IN PLACENTA,
                                                                                     TYPE: PRT
                                                             ORGANISM: Homo sapiens
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o. US20020048763A1
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Hanzel, David K.
Chen, Wensheng
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HIT: AU119728.1, EVALUE 1.00e-38
HIT: BE069876.1, EVALUE 8.00e-03
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RESULT 15
US-09-871-874-11
Sequence 11, Application US/09871874
Patent No. US20020081655A1
GENERAL INFORMATION:
APPLICANT: SAVITZKY, Kinneret
APPLICANT: TOPORIK, Amir
APPLICANT: MINTZ, Liat
TITLE OF INVENTION: Splice Variant of mGluR
FILE REFERENCE: 2786-0176P
CURRENT APPLICATION NUMBER: US/09/871,874
CURRENT FILING DATE: 2001-09-04
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
LENGTH: 401
TYPE: PAT
ORGANISM: Homo sapiens
US-09-871-874-11
Search completed: January 3, 2003, 15:52:07 Job time: 4.77273 secs
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Best Local Similarity 80.0%;
Matches 4; Conservative
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57.944 Million cell updates/sec
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probable membrane	hypothetical prote	H+-exporting ATPas	valine-tRNA ligase	H+-exporting ATPas	valine-tRNA ligase	-trna	valine tRNA synthe	valine tRNA synthe	valine-tRNA ligase	villin - chicken	membrane protein t	galactosylceramida	uracil transport p	hypothetical prote	hypothetical prote

## ALIGNMENTS

R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kon, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: B87530 A;Molecule type: DNA A;Residues: 1-35 <REA> A;Cross-references: GB:AE002165; GB:AE002161; NID:g7188948; PIDN:AAF37906.1; PID:g718 A;Experimental source: strain AR39, HL cells C;Genetics: A;Gene: CP0010 A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39 A;Reference number: A81500; MUID:20150255; PMID:10684935 A;Accession: D81522 R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O., C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Nucleic Acids Res. 28, 1397-1406, 2000 hypothetical protein CP0010 [imported] - Chlamydophila pneumoniae (strain AR39) C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 11-May-2000 C;Accession: D81622 Qγ C;Genetics: A;Gene: CC2267 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-101 <5T0> hypothetical protein CC2267 [imported] - Caulobacter crescentus c;Species: Caulobacter crescentus C;Species: Caulobacter crescentus C;Date: 20-Apr-2001 \*sequence\_revision 20-Apr-2001 #text\_change 20-Apr-2001 C;Accession: B87530 Вþ A; Cross-references: GB:AE005673; NID:g13423780; PIDN:AAK24238.1; GSPDB:GN00148 A; Status: preliminary D81622 Query Match Best Local S Matches 5 Matches Query Match Best Local N 6 VFFWLK 11 1 IFFWIK 6 4; Similarity 5; Conserv Similarity Conservative Conservative 88.9%; 91.7%; 66.7%; 2; Score 32; Pred. No. Score 33; Pred. No. Mismatches Mismatches DB 13; DB 0; Length 35; Length 101; Indels Indels 0; 0,; Gaps Gaps 0.; 0; 0; ; Hicke Salzbe

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conserved hypothetical protein MYPU_4610 [imported] - Mycoplasma pulmonis (strain C;Species: Mycoplasma pulmonis.
C;Date: 24-May-2001 #sequencq_revision 24-May-2001 #text_change 03-Aug-2001 C;Accession: E90569
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A;Title: Complete sequence of the mitochondrial DNA of the rhodophyte Chondrus crispus A;Reference number: S59078; MUID:95341681; PMID:7616569
A;Accession: S59082
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein T03D3.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct.1999 #sequence_revision 29-Oct-1999 #text_change
C;Accession: T32207
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Olecule type: DNA
Residues: 1-374 <MUR>
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Genetic code: SGC3
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||: 17
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5; Conser
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                                                                                                                                                                                                                              88.9%; Score 32; DB 2; llarity 100.0%; Pred. No. 1.2e+(Conservative 0; Mismatches
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hes 0;
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       A; Experimental source:
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A; Molecule type: DNA
A; Residues: 1-660 <KUR>
A; Cross-references: GB: AE008687; PIDN: AAL46227.1;
                                                                                                                                           Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001 A; Authors: Yoo, H.; Tao, Y.; Biddle,
                                                      A; Status: preliminary
                                                                   A; Title: The Genome of the Natural Genetic A; Reference number: AB2577; PMID:11743193 A; Accession: AE3226
                                                                                                                              A; Authors: Yoo, H.; Tao, ster, E.W.
                                                                                                                                                                                                  R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, erage, G.; Gillet, W.; Grant, C.; Guenthner,
                                                                                                                                                                                                                                     conserved hypothetical protein Atu5541 [imported] - Agrobacterium tumefaciens
c;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C;Accession: AE3226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: EM A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Reference number: Z25318; MUID:98083065; PMID:9422602 A;Accession: T51162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Macinga, D.R.; Cook, G.M.; Poole, R.K.; Rather, P.N. J. Bacteriol. 180, 128-135, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Date: 28-Jul-2000 *sequence_revision 28-Jul-2000 *text_change C;Accession: T51162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Species: Providencia stuartii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AL445566; PID:g14089875; A:Experimental source: strain UAB CTIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-423 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: The complete genome sequence of the murine respiratory A;Reference number: A99512; MUID:21267165; PMID:11353084 A;Accession: E90569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Chambaud, I; Heilig, R; Ferris, S. Nucleic Acids Res. 29, 2145-2153, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-544 <MAC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Title: Identification and characterization of aarF, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Bacteriol. 180, 128-135,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aminoglycoside acetyltransferase regulator [imported] - Providencia stuartii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Genetic code:
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ce: strain PR50
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66.7%;
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Pred. No
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Pred. No. 1.4e+02;
2; Mismatches 0;
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                                                                                                                                           P.; Jung,
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                                                                                                          Engineer
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                                                                                                                                             M.; Krespan, W.;
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                                                                                                                                                                                                Kutyavin,
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 PID:g17744003;
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                                                                                                          Agrobacterium
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                                                                                                                                                                                                T.; Levy,
                                                                                                                                                                                                                    Wood,
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 GSPDB:GN00188
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strain C58 (Dupont)

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A:Molecule type: DNA
A:Residues: 1-988 <COL>
A:Residues: 1-988 <COL>
A:Cross-references: GB:AE001212; GB:AE000520; NID:g3322597; PIDN:AAC65312.1; PID:g332266
A:Cross-referental source: strain Nichols
C:Genetics:
A:Gene: TP0325
A:Gene: TP0325
C:Superfamily: syphilis spirochete conserved hypothetical protein TP0325
                               Qy
                                                                                                                                                 C; Genetics:
A; Gene: STY3003
                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-86 <PAR>
                                                                                                                                                                                                                                                                           R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Ch th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Steve A;Title: Complete genome sequence of a multiple drug resistant Salmonella enteric A;Reference number: AB0502; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            conserved hypothetical protein TP0325 - syphilis spirochete C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete) C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 21-Jan-2000 C:Accession: H71338
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A;Gene: Atu5541
                                                                                                                                                                                  A;Cross-references: GB:AL513382; PIDN:CAD05987.1; PID:g16503958; GSPDB:GN00176
                                                                                                                                                                                                                                                               A; Reference number: A; Accession: AD0850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
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                                                                        Matches
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Best Local
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Best Local
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bte: this species has also been called Salmonella typhi
ate: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
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es 5; Conserv
53 LFYWIK 58
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                                                                                          Similarity
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Conservative
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                                                                                          86.1%;
66.7%;
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A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: D69381
                         R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, J. DNA Res. 8, 205-213, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Fulton, R.; Hawkins, J.; Rohlfing, T. submitted to the EMBL Data Library, October 1998 A;Description: The sequence of C. elegans cosmid F43B10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein F43B10.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 04-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; nucleic acid sequence not shown; translation A;Molecule type: DNA A;Residues: 1-162 <KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
                                                                                                                    A;Note: Nostoc sp. strain PCC 7120 is a synonym of C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position:
A; Introns: 88/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession:
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                                                                                               C; Accession: AG2542
                                                                                                                                                                     hypothetical protein all7626 [imported] - Nostoc sp. (strain PCC 7120) plasmid C; Species: Nostoc sp.
                                                                                                                                                                                                                                                     RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: CESP:F43B10.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: EMBL: AF098500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-247 <FUL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein AF1052 - Archaeoglobus fulgidus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Map position: X
;Introns: 88/2; 103/3; 128/3
;Superfamily: Caenorhabditis elegans hypothetical protein F43B10
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100.0%; Pr
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Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
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Pred. No. 1.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIDN:AAC67400.1; GSPDB:GN00028; CESP:F43B10.1 tol N2; clone F43B10
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                                                                                                                    Anabaena sp. strain PCC 7120
#text_change 30-Jun-2002
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                                                   Yasuda, M.;
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A;Cross-references: GB:AE001802; GB:AE000512; NID:g4982133; PIDN:AAD36643.1; PID:g498214
A:Experimental source: strain MSB8
C:Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: S74322; MUID:97061201; PMID:8905231
A; Accession: S75891
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C:Accession: S75891
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu. E. Nakamura v. P
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A;Genome:
                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-267 < ARN>
                                                                                                                                                                                                                                                                                                                                                         hemolysin - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: A72238
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Best Local Similarity
Thehes 5; Conserv
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                                                                                                                                                                                                         A; Status: preliminary
                                                                                                                                                                                                                             A; Reference number: A72200; A; Accession: A72238
                                                                                                                                                                                                                                                                                                                  R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hi Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           망
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A; Residues: 1-258 < KUR>
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Query Match
Best Local Similarity
                                                                         ;Gene: TM1576
;Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Accession: $75891; Accession: $75891; Accession: $75891; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Kaneko, T.; Sato, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; NA Res. 3, 109-136, 1996
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5; Conserv
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                                                                                                                                                                                                                                            lateral gene transfer between Archaea 72200; MUID:99287316; PMID:10360571
                                                                       homolog yqxC
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100.0%;
                   86.18;
80.08;
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Pred.
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Pred. No.
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                 31;
No.
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3. 1.3e+02;
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J. 1.3e+02;
O;
                 DB 2;
1.3e+02;
                                  Length 267
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Yamada, M.; Yasuda
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1996
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R; Bevan, M.; Terryn, N.; Ardiles, W.; Buysshewes, H.W.; Mayer, K.F.X.; Schueller, C. submitted to the Protein Sequence Database,
                                                       В
                                                                               Qy
                                                                                                                                                                A; Map position: 4
A; Introns: 37/2; 116/2;
A; Note: F1C12.211
                                                                                                                                                                                                                                                                                                                                              hypothetical protein F1C12.211 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999 C;Accession: T05338
                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
Search completed: January Job time: 10.9545 secs
                                                                                                                                                                                                          A; Experimental source: cultivar C; Genetics:
                                                                                                                                                                                                                      A;Cross-references: EMBL:AL022224
A;Experimental source: cultivar Columbia; BAC
                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-287 <BEV>
                                                                                                                                                                                                                                                                             A; Reference number: 215408
A; Accession: T05338
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16-0CT-2001
16-0CT-2001
16-0CT-2001
            Chloroplast.
Eukaryota; Viridiplantae;
                                                    Mesostigma viride.
                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
NADH-plastoquinone oxidoreductase chain 1, chloroplast
                                                                                                                                                      Q9MUL1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Mesostigmatales; Mesostigmataceae;
                                                                     NDHA
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE001030; AAB90193.1; TIGR; AF1052; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein; Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
STRAIN-VC-16 / DS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=VC-16 / DSM 4304 / ATCC 49
MEDLINE=98049343; PubMed=9389475;
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(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                      STANDARD;
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50.0%;
               Streptophyta; Mesostigmatophyceae;
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Pred. No.
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Mesostigma
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Best Local
EPR SPECTROSCOPY.

EPR SPECTROSCOPY.

STRAIN-ATCC 14405 / Zobell;

MEDLINE-98191362; PubMed-9521721;

Cheesman M.R., Zumft W.G., Thomso
                                                                                                                                                                                                   Zumft W.G., Braun C., Cuypers H.;
"Nitric oxide reductase from Pseudomonas stutzeri. Primary structure and gene organization of a novel bacterial cytochrome bc complex.";
Eur. J. Biochem. 219:481-490(1994).
                                                                                                                                                                                                                                                       SIRAIN-ATCC 14405
MEDLINE-94139726;
Zumft w C
                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Nitric-oxide reductase subunit B (EC 1.7, 99.7)
                                                                                                        cytochrome
                                                                                                                                                                 EPR SPECTROSCOPY.
STRAIN-ATCC 14405
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Pseudomonas.
                                                                             J. Bacteriol.
                                                                                                                        "Formation
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                                                                                                                                                  MEDLINE-89255095;
                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas stutzeri (Pseudomonas perfectomarina)
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                                                                                                                                                                                                                                                                                                                                                                                              cytochrome b subunit) (NOR large subunit).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lemieux C., Otis C., Turmel M.;
"Ancestral chloroplast genome in Mesostigma viride reveals an early branch of green plant evolution.";
Nature 403:649-652(2000).
-i- CATALYTIC ACTIVITY: NADH + plastoquinone - NAD(+) + plastoquinol.
-i- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 1 FAMILY.
                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=316;
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PROSITE; PS00668; COMPLEX1_ND1_2;
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Frunzke K., Zumft W.G.;
n of the N-N bond from nitric oxide by
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40369 MW; 158CF9E44A58EB98 CRC64;
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                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                     gamma subdivision; Pseudomonadaceae;
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Pred. No.
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pred. No. 85;
Mismatches
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Thomson A.J.;

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RESULT 5
NU4M_MARPO
ID NU4M_MARPO
AC P26848;
DT 01-FEB-1994
DT 01-FEB-1994
DT 01-FEB-1994
DT 01-FCB-1996
DE NADH-ubiquir
GN NADH-ubiquir
GN NADH-ubiquir
GN NADH-ubiquir
GN MATChantia |
OG Mitochondria |
OG Eukaryota;
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Best Local
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01-FEB-1994
01-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                   O1-FEB-1996 (Rel. 33, Last annotation update) NADH-ubiquinone oxidoreductase chain 4 (EC 1.6.5.3).
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METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   structurally related to the heme-copper oxidases.";
Biochemistry 37:3994-4000(1998).
-!- FUNCTION: COMPONENT OF THE ANAEROBIC RESPIRATORY CHAIN THAT TRANSFORMS NITRATE TO DINITROGEN (DENITRIFICATION). NORB IS
  Eukaryota; Viridiplantae;
               Mitochondrion
                          Marchantia polymorpha
                                        ND4 OR NAD4.
                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTIVITY ACROSS THE MEMBRANE IN DENITRIFYING BACTERIAL CELLS. THE MONONITROGEN REDUCTION IS PROBABLY COUPLED TO ELECTRON TRANSPORT
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66.7%;
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Last annotation updat
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 Streptophyta; Embryophyta; Marchantiophyta;
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                                                                                                                                                                                                                                                                                      NU4M_ACACA
Q37375;
15-JUL-1998
                       castellanii: complete sequence, organization.";
J. Mol. Biol. 245:522-537(1995).
-!- CATALYTIC ACTIVITY: NADH + u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oda K., Yamato K., Ohta E., Nakamura Y., Takemura M., Nozato N., Akashi K., Kanegae T., Ogura Y., Kohchi T., Ohyama K.; "Gene organization deduced from the complete sequence of liverwort Marchantia polymorpha mitochondrial DNA. A primitive form of plant mitochondrial genome."; J. Mol. Biol. 223:1-7(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001750; Oxidored_q1. pfam; PF00361; Oxidored_q1; 1. PRINTS; PR01437; NUXDRDTASE4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Cotranscriptional expression of mitochondrial genes for subuni NADH dehydrogenase, nad5, nad4, nad2, in Marchantia polymorpha. Mol. Gen. Genet. 237.343-350(1993).
-i- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
This SWISS-PROT entry is copyright.
                                                                                   Burger G., Plante I., Lonergan K.M., Gray M.W.; "The mitochondrial DNA of the amoeboid protozoo
                                                                                                                STRAIN=ATCC 30010 MEDLINE=95147275;
                                                                                                                                                                                      Eukaryota; Acanthamoebidae;
                                                                                                                                                                                                    Mitochondrion.
                                                                                                                                                                                                                               ND4 OR NAD4
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InterPro; IPR003918; NADHub_oxred4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. Thuse by non-profit institutions as long
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                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                       NCBI_TaxID=5755;
                                                                                                                                                                                                                 Acanthamoeba castellanii (Amoeba).
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1. 36, Last sequence update)
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oxidoreductase chain 4 (EC 1.
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PubMed=7844823;
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56311 MW; OI
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66.7%;
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                          ubiquinone = .NAD(+) + ubiquinol
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                                                MEDIJINE-MEZ280759; PubMed-Javv, ... MIShihara M., Winters C.A., Buzko E., Nishihara M., Winters C.A., Buzko E., "Hormonal regulation of rat Leydig ce "Hormonal regulation of a part
                                                                                                                                                                             STRAIN-Sprague-Dawley;

MEDLINE-95217329; PubMed=7702752;

Givens C.R., Zhang P., Bair S.R., Mellon S.H.;

Givens C.R., Zhang P., Bair S.R., Mellon S.H.;

"Transcriptional regulation of rat cytochrome P450c17 expression in mouse Leydig MA-10 and adrenal Y-1 cells: identification of a single protein that mediates both basal and cAMP-induced activities.";

DNA Cell Biol. 13:1087-1098(1994).
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P11715;
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Namiki M., Kitamura M., Buczko E., Dufau M.L.;
"Rat testis P-450(17)alpha cDNA: the deduced amino expression and secondary structural configuration."
Blochem. Blophys. Res. Commun. 157:705-712(1988).
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MEDLINE=89295447; PubMed=2786990;
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Mammalia; Eutheria; Rodentia;
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01-AUG-1990 (Rel. 15, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Cytochrome P450 17 (EC 1.14.99.9) (CYPXVII) (P450-C17) (Steroid
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Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SEQUENCE 497 AA; 57768 MW; 9C0B637E65C0E3B5 CRC64;
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                                                                                                                                               OF 271-507
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Bioinformatics Institute. There are no restrictions
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P38196;
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Mellon S.H., Vaisse C.;
"CAMP regulates P450scc gene expression by
"CAMP regulates P450scc gene expression by
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FUI1 OR YBL042C OR YBL0406
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        MEDLINE-95176707; PubMed-7871888;
                                                 STRAIN=S288c
                                                                                  SEQUENCE FROM
                                                                                                                                                                                                     Eukaryota; Fungi;
Saccharomycetales;
                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
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MEDLINE=90046678;
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Pfam; PF00067; p450; 1.
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; A30828; A30828.
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FUNCTION: CONVERSION OF PREGNENOLONE AND PROGESTERONE TO
17-ALPHA-HYDROXYLATED PRODUCTS AND SUBSEQUENTLY TO
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Galactocerebrosidase precursor (EC 3.2.1.46) (GALCERASE)
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Vickers M.F., Yao S.Y., Baldwin S.A., Young J.D., Cass C.E.;
"Nucleoside transporter proteins of Saccharomyces cerevisiae."
Pemonstration of a transporter (FUI1) with high uridine selectivity in plasma membranes and a transporter (FUN26) with broad nucleoside selectivity in intracellular membranes.";
J. Biol. Chem. 275:25931-25938 (2000).
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Wagner R., de Montigny J., de Wergifosse P.,
"The ORF YBL042 of Saccharomyces cerevisiae
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01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Galactocerebrosidase precursor (EC 3.2.1.46) (
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                                                                                                                                                                                                                                  GALC_HUMAN P54803;
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Pfam; PF02057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed.
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Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
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                           (Galactocerebroside beta-galactosidase). GALC.
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LEUKODYSTROPHY (GLD). THIS DEFICIENCY RESULTS IN THE IN:
CATABOLISM OF SEVERAL GALACTOLIPIDS THAT ARE IMPORTANT 1
PRODUCTION OF NORMAL MYELIN.
SIMILARITY: BELONGS TO FAMILY 59 OF GLYCOSYL HYDROLASES
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CATALYTIC ACTIVITY: D-galactosyl-N-acylsphingosine + H(2)0
galactose + N-acylsphingosine.

SUBCELLULAR LOCATION: Lysosomal (By similarity).
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"Molecular genetics of Krabbe disease (globoid cell leukodystrophy):
diagnostic and clinical implications.";
Hum. Mutat. 10:268-279(1997).
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Luzi P., Rafi M.A., Wenger D.A.;
"Structure and organization of the human galactocerebrosidase (GALC)
                                                                                                                                                                                                                                                                                           Rafi M.A., Luzi P., Zlotogora J., Wenger D.A.; "Two different mutations are responsible for Krabbe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Okada S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tatsumi N., Inui K., Sakai N., Fukushima H.,
Yanagihara I., Nishigaki T., Tsukamoto H., F
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"Cloning and expression of cDNA encoding human galactocerebrosidase,
the enzyme deficient in globoid cell leukodystrophy.";
Hum. Mol. Genet. 2:1841-1845(1993).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Yanagihara I., Isegawa Y., Iwamatsu A., Okada S.;
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Hum. Mol. Genet. 4:1865-1868(1995).
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Tatsumi N., Ozono K., Okada S.;
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o different mutations are responsible.";

ze and Moslem Arab populations in Israel.";

ze and Moslem Arab (1996).

FUNCTION: HYDOLYSES THE GALACTOSE ESTER BONDS OF FUNCTIONE, AND MONOCALACTOSYLCERAMIDE, GALACTOSYLSEMIDE, ENZYME WITH VERY LOW ACTIVITY RESPONSIBLE FOR THE LYSOSOMAL CATABOLISM OF GALACTOSYLCERAMIDE, MAJOR LIPID IN MYELIN, KIDNEY AND EPITHELIAL CELLS OF SMALL INTESTINE AND COLON. HAS AN OPTIMAL PH BETWEEN 4.0 AND 4.4.

INTESTINE AND COLON. HAS AN OPTIMAL PH BETWEEN 4.0 AND 4.4.
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ma H., Inui K., Fu
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galactose + N-acylsphingosine.
-!- SUBCELLULAR LOCATION: Lysosomal.
-!- ALTERNATIVE PRODUCTS: TWO FORMS ARE PRODUCED BY ALTERNATIVE SUBCELLULAR LOCATION: Lysosomal.
-!- TISSUE SPECIFICITY: HIGHEST LEVEL OF ACTIVITY IN TESTES COMPARED TO BRAIN, KIDNEY, PLACENTA AND LIVER. CAN ALSO BE FOUND IN URINE.
-!- DISEASE: DEFECTS IN GALC ARE THE CAUSE OF GLOBOID CELL
LEUKODYSTROPHY (GLD) (OR KRABBE DISEASE). THIS AUTOSOMAL RECESSIVE DISCADES DEFICIENCY RESULTS IN THE INSUPFICIENT CATABOLISM OF SEVERAL GALCATOLIPIDS THAT ARE IMPORTANT IN THE PRODUCTION OF NORMAL MYELLN. CLINICALLY THE MOST FREQUENT FORM IS THE INFANTILE FORM. MOST PATIENTS (90%) PRESENT BEFORE SIX MONTHS OF AGE WITH IRRITABILITY, SPASTICITY, ARRESTO OF MOTOR AND MENTAL DEVELOPMENT, AND BOUTS OF TEMPERATURE ELEVATION WITHOUT INFECTION. THIS IS FOLLOWED BY MYOCLONIC JERKS OF ARMS AND LEGS, OPOSTHOTONUS, HYPERTONIC FITS, AND MENTAL REGRESSION, WHICH PROGRESSES TO A SEVERE DECEREBRATE CONDITION WITH NO VOLUNTARY MOVEMENTS BEFORE 2 YEARS OF AGE. HOWEVER, A SIGNIFICANT NUMBER OF CASES WITH LATER ONSET, PRESENTING WITH UNEXPLAINED BLINDNESS, WEAKNESS AND/OR PROGRESSIVE MOTOR, AND SENSORY NEUROPACHY THAT CAN PROGRESS TO SEVERE MENTAL INCAPACITY AND DEATH, HAVE BEEN IDENTIFIED.
-!- SIMILARITY: BELONGS TO FAMILY 59 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
Galactocerebrosidase precursor (EC 3.2.1.46) (GALCERASE)
(Galactosylceramidase) (Galactosylceramide beta-galactosidase)
(Galactocerebroside beta-galactosidase).
 SEQUENCE FROM N.A.
MEDLINE=97336058; PubMed=9192853;
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Mammalia; I
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Pred. No.
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/FTId=VAR_003392.
P -> A (IN GLD).
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N -> T (IN GLD).
/FTId=VAR_003391.
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D -> V (IN GLD).
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T -> A (IN GLD; A
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/FTId=VAR_003380.
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                                    Craniata; V
Catarrhini;
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1.5e+02;
                                    Vertebrata; Euteleostomi;
i; Cercopithecidae;
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RESULT 12
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ID ATY3_HUMAN
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5; Conserv
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                                                                      Score 31; DB; Pred. No. 1.5
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SIMILARITY.

(POTENTIAL).
(POTENTIAL).
(POTENTIAL).

(POTENTIAL) (POTENTIAL) (POTENTIAL)

PRT;

684

A

DB 1; 1.5e+

Length 669; CRC64;

.5e+02;

Indels

0;

Gaps

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use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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-(CATALYTIC ACTIVITY: D-galactosy)-N-acylsphingosine + H(2)
galactose + N-acylsphingosine.

-(CATALYTIC ACTIVITY: D-galactosy)-N-acylsphingosine + H(2)
galactose + Location: Lysosomal (By similarity).

-(CATALYTIC ACTION: Lysosomal 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Luzi P., Rafi M.A., Victoria T., Baskin G.B., Wenger D.A.; "Characterization of the rhesus monkey galactocerebrosidase "DNA and gene and identification of the mutation causing glo leukodystrophy (Krabbe disease) in this primate."; Genomics 42:319-324(1997).
                                                                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN 
European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: HYDROLYSES THE GALACTOSE ESTER BONDS OF GALACTOSYLCERAMIDE, GALACTOSYLSPHINGOSINE, LACTOSYLCERAMIDE, AND MONOGALACTOSYLCERAMIDE. ENZYME WITH VERY LOW ACTIVITY.

RESPONSIBLE FOR THE LYSOSOMAL CATABOLISM OF GALACTOSYLCERAMIDE, AMAJOR LIPID IN MYELIN, KIDNEY AND EPITHELIAL CELLS OF SMALL
                                                            (See http://www.isb-sib.ch/announce/
                                                                                                                                                                              as its content
                                                                                                                        Usage
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DEFICIENCY
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                                         Bacteria; Proteobacteria;
                                                                                    TraD
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16-OCT-2001
                                                                                                                             TRD1_ECOLI P09130;
                                                                                                                                                                                                                                                                                                                                                                             NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Sh
Tanaka T., Nakamura Y., Isogai T., Sugan Os.;
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + H(2)0 = ADP + phosphate.
-!- SUBCELLUIAR LOCATION: Integral membrane protein (By
SEQUENCE
                               Escherichia
                                                    Plasmid F.
                                                              Escherichia
                                                                                                                 01-MAR-1989
                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed.
                    NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AK024639; BAB14942.1; ALT_INIT.
InterPro; IPR001757; ATPase_E1-E2.
InterPro; IPR001454; H1gnase/hydrlase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-OCT-2002 (Rel. 41, Last annotation update)
Probable cation-transporting ATPase 3 (EC 3.6.3.-) (Fragment).
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TISSUE-Coronary ar
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Eukaryota; Metazoa; (
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                                                                                  protein
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FROM
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684 AA;
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Primates;
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annotation
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Pred. No.
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MAGNESIUM (BY SIMILARITY).
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                                         Enterobacteriaceae;
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Lee M.H., Kosuk N., Bailey J., Traxler B., Manc "Analysis of F factor TraD membrane topology by and trypsin sensitive insertions.";
J. Bacteriol. 181:6108-6113(1999)
-i- FUNCTION: TRAD IS A CELL ENVELOPE PROTEIN.
IS UNKNOWN BUT IT IS ESSENTIAL FOR DNA TRAN MAY BE PART OF A NON-SPECIFIC PORE FOR DNA
                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-90317835; PubMed-2164585; Yoshioka Y., Fujita Y., Ohtsubo E.; Yoshioka Y., Fujita Y., Ohtsubo E.; "Nucleotide sequence of the promoter-distal re of plasmid R100, including tral (DNA helicase J. Mol. Biol. 214:39-53(1990).
                                                                                                                                                                                                                                                                                                                  Panicker M.M., Minkley E.G. Jr.;
"Purification and properties of the F sex factor TraD protein, inner membrane conjugal transfer protein.";
J. Biol. Chem. 267:12761-12766(1992).
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J. Mol. Biol. 198:1-11(1987).
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the F sex
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-K12 / CR63;
Shimizu H., Saitoh
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    Bacteriol.

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                                                                                                                      SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: TO THE TRAD OF PLASMID INCFII R100.
                                                                                                                                                      DIRECTLY ENERGIZES DNA TRANSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81:195-202(1989).
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01-AUG-1991
15-DEC-1998
                                                                          SEQUENCE FROM N.A.

MEDLINE-90317835; PubMed=2164585;

YOShioka Y., Fujita Y., Ohtsubo E.;

Yoshioka Y., Fujita Y., Ohtsubo E.;

Yoshioka Y., Fujita Y., Ohtsubo E.;

Youclectide sequence of the promoter-distal region of the tra

of plasmid R100, including trai (DNA helicase I) and traD gen

of plasmid R100, including trai (DNA helicase I) and traD gen

J. MOI. Biol. 214:39-53(1990).

-i- FUNCTION: TRAD IS A CELL ENVELOPE PROTEIN. THE FUNCTION O

IS UNKNOWN BUT IT IS ESSENTIAL FOR DNA TRANSPER. IT MAY F

MAY BE PART OF A NON-SPECIFIC PORE FOR DNA EXPORT, OR IT

DIRECTLY ENERGIZES DNA TRANSPORT.
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S01758; S01758.
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non-profit institutions as long and this statement is not removed
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P02640;
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J. Biol. Chem. 256:8156-8161(1981).
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MEDLINE=88276884; PubMed=2839826;
Bazari W.L., Matsudaira P., Wallek M.,
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Enkarvota; Metazoa; Chordata;
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PIR; S
                actin-severing domains.";
Protein Sci. 6:1197-1209(1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam;
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                                                      Markus M.A., Matsudaira P., Wagner G 
"Refined structure of villin 14T and
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                                                                                                                                                                          severing
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"Demonstration of three distinct calcium-binding
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sci. 3:70-81(1994).
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"NMR structure of the 35-residue villin headpiece subdomain.";

Nat. Struct. Biol. 4:180-184(1997).

-i- FUNCTION: CA(2+)-REGULATED ACTIN-BINDING PROTEIN. ITS CAPPING FUNCTION IS LOCALIZED TO DOMAIN I; ITS SEVERING ACTION IS A COOPERATION BETWEEN AN F-ACTIN BINDING SITE OF DOMAIN II AND THE CAPPING ACTIVITY OF DOMAIN I.

-i- SUBUNIT: MONOMER.
-i- TISSUE SPECIFICITY: COMPONENT OF BRUSH BORDER MICROVILLI.
-i- SIMILARITY: CONTAINS 6 GELSOLIN-LIKE REPEATS.
                                                   SEQUENCE
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GELSOLIN-LIKE 5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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~~**eria; Proteobacteria;
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EMBL; AY005138; AAG12430.1; -. ABFEF8FCF70B7411
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Bauer B.A., Lumbley S.R., Hansen E.J.;
"Characterization of a Waaf (Rfaf) hom
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Bacteria; Chlorobi;
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MEDLINE-94167241; PubMed-8121799;

Schnitzler P., Hug M., Handermann M., Janssen Delius H., Darai C.;

"Identification of genes encoding zinc finger chromosomal HMG protein homologue, and a putat in the genome of Chilo iridescent virus.";

Nucleic Acids Res. 22:158-166(1994).
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE-92196996; PubMed-1549908;

"--darmann M., Schnitzler P., Ros
                                                                                                                                                   Stohwasser R., Raab K., Schnitzler P., Janssen W., "Identification of the gene encoding the major caps insect inidescent virus type 6 by polymerase chain J. Gen. Virol. 74:873-879(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-89073752; PubMed-3201750;
Fischer M., Schnitzler P., Delius H., Darai G.;
"Identification and characterization of the repetitive
the genome of insect iridescent virus type 6.";
Virology 167:485-496(1988).
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"DNA analysis of insect iridescent vir
permutation and terminal redundancy.";
J. Virol. 49:609-614(1984).
                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE-93260401; PubMed-8492091;
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MEDLINE-87321126; PubMed-2820141;
Schnitzler P. Soltau J.B., Fischer M.,
Delius H., Darai G.;
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Darai G.,
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Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Iridovirus
                SEQUENCE FROM N.A
                                                                                                                                                                                                                                     "Characterization of the third origin of DNA replication of insect iridescent virus type 6."; Virus Genes 6:333-342(1992).
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"Analysis of the First Complete DNA Sequence Iridovirus: Coding Strategy of the Genome of Virology 286:182-196(2001).
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"The DNA sequence of Chilo iridescent virus between coordinates 0.101 and 0.391; similarities in coding insect and vertebrate iridoviruses.";
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J. Gen. Virol. 75:1557-1567(1994).
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STRAIN-ATCC 19089 / CB15;
MEDLINE-21173698; PubMed=11259647;
MIETMAN W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K. Rieman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson W.C., Newton A., Stephens C., Phadke N.D., El DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., Whi Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.; "Complete genome sequence of Caulobacter crescentus."; proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
                                                              TIGRFAMs; Flagella.
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apparatus.";
Submitted (MAR-2000)
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01-MAR-2002 (TrEMBLrel. 20, L
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Lactobacillus delbrueckii (su
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J. Mol. Evol. 41:196-202(1995).
EMBL; 247547; CAA87598.1;
                                                                                Bourniquel A.A., Casey M.G., Mollet B., "DNA sequence and functional analysis o subsp. lactis plasmids pN42 and pJBL2." Plasmid 0.0-0(0).
EMBL; AJ421486;
Plasmid.
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Leblanc C., Boyen
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NCBI_TaxID=29397;
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C., Richard O.,
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Rohu liver hypothetical protein (Fragment).
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                                         Hypothetical protein; Complete SEQUENCE 120 AA; 14167 MW;
                                                            May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam "Complete genomic sequence of Pasteurella multocida Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
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                                                                                                                                                                  Bacteria; Proteobacteria;
                                                                                                                                                                           Pasteurella multocida
                                                                                                                                                                                       PM0679
                                                                                                                                                                                                 Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                     MEDLINE-21145866; PubMed-11248100;
                                                                                                                                            NCBI_TaxID=747;
                                                                                                                                                        Pasteurella
                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
                                                                                                                         EQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94 LFFWLK 99
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es 4; Conser
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                                                                                                                                                                                                                                                                                                                                            88.9%; ilarity 100.0%; Conservative
  Conservative
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          100.0%;
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                     88.9%;
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46308C480002FF64 CRC64;
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                                                                                                                                                                  subdivision; Pasteurellaceae;
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                      DB 16;
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            1.3e+02;
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Matches 4
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O1-MAR-2002 (TrEMBLrel. 20, Created)

O1-MAR-2002 (TrEMBLrel. 20, Last sequence up

O1-MAR-2002 (TrEMBLrel. 20, Last annotation

Hypothetical 19,6 kDa protein,

Lactobacillus delbrueckii (subsp. lactis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q916G8 PRELIMINARY; PRT; 1/4 AA.
Q916G8;
Q1-QCT-2000 (TrEMBLrel. 15, Created)
Q1-QCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-QCT-2000 (TrEMBLrel. 15, Last annotation update)
  Q98QA5
                                                                                                                                                                                                                                                                                                                                                                                              Plasmid 0:0-0(0).
Plasmid 0:0-0(0).
EMBL; AJ421627; CAD15746.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Bourniquel A.A., Casey M.G., Mollet B.,
"DNA sequence and functional analysis of
subsp. lactis plasmids pN42 and pJBL2."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90NA8Ö
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"Structural analysis of pLBB1, a cryptic plasmid from Ladelbrueckii subsp. bulgaricus.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lactobacillaceae;
NCBI_TaxID=29397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillus/Clostridium Lactobacillaceae; Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmid pN42.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF236060; AAF61726.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Bacillus/C
Lactobacillaceae; Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmid pLBB1.
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                                                                                                                                                                                                                                             4.
                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                             Conservative
  PRELIMINARY;
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                                                                                                                                                                                                                                                                   Score 32;
Pred. No.
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Pred. No. 1.8e+02;
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  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      B., Pridmore R.D.;
s of Lactobacillus c
2.";
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01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                           Universidad de Salamanca.
-!- SIMILARITY: BELONGS TO THE SER/THR EMBL; AJ298993; CAC09581.1; -
                                                                                                                                                                                                                                                                               Lorenzo O., Rodriguez D., Nicolas C., Ni
"Characterization and expression of two
like gene, which are regulated by ABA ar
sylvatica seeds.";
                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Stro
Spermatophyta; Magnoliophyta;
eurosids I; Fagales; Fagaceae
                                                                                                                                                                                                                                           (In) Black M., Bradford K.J., Vazquez-Ramos SEED BIOLOGY-ADVANCES AND APPLICATIONS 32, p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9FDV6
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Hypothetical protein; Complete proteome.

SEQUENCE 423 AA; 50819 MW; B4A027C3E9264F9E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycoplasma pulmonis.
Nucleic Acids Res. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21267165; PubMed=11353084;
Chambaud I., Heilig R., Ferris S., Barbe V., S
Moszer I., Dybvig K., Wroblewski H., Viari A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycoplasmataceae; NCBI_TaxID=2107;
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01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0UN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein MYPU_4610.
         InterPro;
                      InterPro;
                                         InterPro;
                                                                                                                                    Thesis (2000),
                                                                                                                                                                        TISSUE=SEED;
                                                                                                                                                                                                                             CAB international,
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                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=28930;
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                                                            InterPro;
                                                                                                                                                     Lorenzo O
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IPR001064; Crystallin.
IPR000719; Euk_pkinase.
IPR0002290; Ser_thr_pkinase.
IPR001245; Tyr_pkinase.
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IPR004477; ComEC_N-term.
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/ta; eudicotyledons;
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Pred. No.
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and GA3 in dormant Fagu
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pp.329-340,
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"Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58.";
Science 294:2323-2328(2001).
EMBL; AE008974; AAL46227.1; ALT_INIT.
EMBL; AE007922; AAK90918.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D. Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Kutyavin T., Cevy R., Li M.-J., McClelland E., Palmieri A., Gordon I., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V., Mester E.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein Atu5541.
ATU5541 OR AGR_PAT_807.
Agrobacterium tumefaciens (strain C58 / ATCC 33970).
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SMART; SM00220; S_TKC; 1.

SMART; SM00219; TyrKC; 1.

PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.

PROSITE: PS00101; PROTEIN_KINASE_DOM; 1.

PROSITE: PS00108; PROTEIN_KINASE_ST; 1.

ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.

SEQUENCE 666 AA; 74385 MW; DA586B1276259C97 CRC64;
                                                                                                                                        Hypothetical protein; Plasmid; Complete proteome. SEQUENCE 671 AA; 72766 MW; 43EDB89528813482 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 294:2317-2323(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The genome of the natural genetic engineer Agrobacterium tumefaciens {\sf C58."};
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=21608550; PubMed=11743193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
NCBI_TaxID=176299;
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369 IFFWIE 374
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                                 1 IFFWIK 6
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Search completed: January 3, 2003, 15:32:03 Job time: 21.3182 secs

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Maximum Match 100%
Listing first 45 summaries
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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2 US-08-068-392-2

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4 US-08-915-429-2

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6 US-08-911-114

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SEQUENCE CHARACTERISTICS:
LENGTH: 3287 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-451-7

Query Match Best Local Similarity Thehes 5; Conserv

Conservative

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94.4%;

Score 34; DB 2; Pred. No. 5.5e+02; Mismatches

Length 3287; Indels

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1 IFFWIK 6 IFFWLK 684

RESULT 1 US-08-477-451- Sequence 7, Patent No. 5; GENERAL INF APPLICANT TITLE OF NUMBER OF CORRESPON ADDRESS; STRATE: CITY: STRATE: COUNTRY ZIP: COMPUTER MEDIUM COMPUTER MEDIUM SOFTWAR CURRENT A APPLICA FILING FILING FILING REFEREN	2000 2000 2000 2000 2000 2000 2000 200	
-7 Application US/08477451 5928865 FORMATION: T: Covacci, Antonello INVENTION: Helicobacter Pylori Cagi F SEQUENCES: 46 NDENCE ADDRESS: SEE: Chiron Corporation : 4560 Horton Street Emeryville CA Y: USA 94608-2916 READABLE FORM: TYPE: Floppy disk TYPE: Floppy disk ER: IBM PC compatible ING SYSTEM: PC-DOS/MS-DOS RE: PATENTIN Release #1.0, Version #1 APPLICATION DATA: APPLICATION 1995 FICATION 1995 FICATION 1995 FICATION NUMBER: U35/08/477,451 DATE: 07-JUN-1995 FICATION 1995 FICATION NUMBER: 33,113 NCE/DOCKET NUMBER: 035.002 UNICATION INFORMATION: ONE: 510-605-3542 N FOR SEQ ID NO: 7:	29 80.6 505 3 US-08-747-221B-14 29 80.6 505 4 US-09-005-051-14 29 80.6 530 3 US-08-747-221B-53 29 80.6 530 4 US-09-005-051-53 29 80.6 550 3 US-08-747-221B-59 29 80.6 550 4 US-09-005-051-58 29 80.6 550 4 US-09-005-051-58 29 80.6 776 4 US-09-105-051-58 29 80.6 1298 1 US-08-22-616-33 29 80.6 1298 1 US-08-340-011-2 29 80.6 1298 3 US-08-340-011-2 29 80.6 1298 4 US-08-916-33 29 80.6 1298 5 PCT-US95-04228-33 29 80.6 1362 3 US-08-874-678-33 29 80.6 1362 3 US-08-643-839-33 29 80.6 1362 3 US-08-643-839-33 29 80.6 1363 1 US-08-340-011-4	
Region	Sequence 14, Appl Sequence 33, Appl Sequence 53, Appl Sequence 59, Appl Sequence 19, Appl Sequence 58, Appl Sequence 3, Appl Sequence 3, Appl Sequence 2, Appli Sequence 2, Appli Sequence 33, Appl Sequence 33, Appl	

APPLICATION NUMBER: PCT/US95/06725

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RESULT 3
PCT-US95-06725-4
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GENERAL INFORMATION:
APPLICANT:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/253,
FILING DATE: 03-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: DIG19110, Frank S.
REGISTRATION NUMBER: 31,346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acids
TYPE: amino acid
TOPOLOGY: 11--
CURRENT APPLICATION DATA:
                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                          TITLE OF INVENTION: LA
TITLE OF INVENTION: LO
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 93
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                           118 VFFWI 122
            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                      CITY: Garden City
STATE: New York
                                                                                                                                                                         ADDRESSEE: Scully, Scott, Murphy & Presser STREET: 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity les 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Garden City
STATE: New York
                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
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                                                                                                         11530
                                                                                                                                                                                                                                                                                                                     Application PC/TUS9506725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jazwinski, S. M.
VENTION: LAG1:
                                                                                                                      United States
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                                                                                                                                                                                                                                              LAG1: A GENE FOR INCREASING THE LONGEVITY OF EUKARYOTES
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Pred. No.
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2e+02;
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US-08-336-031-2
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Best Local Similarity
Matches 4; Conserv
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INFORMATION FOR SEQ ID NO:
                                                                                          TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                         CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
PTITING DATE: 03-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING CALLS
CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 08/253,875 & 08/336,031
APPLICATION NUMBER: US 08/253,875 & 08/336,031
APPLICATION NUMBER: 03-JUN-1994 & 08-NOV-1994
                                                                                                                                                                                                            AFFLIANCE O3-JUN-155.
FILING DATE: 03-JUN-155.
ATTORNEY/AGENT INFORMATION:
NAME: D1G1g110, Frank S.
NAME: D1G1g110, Frank S.
NAME: D1G1g110, Frank S.
                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                 REFERENCE/DOCKET NUMBER: 9303Z TELECOMMUNICATION INFORMATION: (516) 742-4343
                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,031
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LENGTH: 218 amino acid
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MOLECULE TYPE:
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                                 TYPE: amino acid
                                                                                                                                                                                                      REGISTRATION NUMBER: 31,346
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                                                     LENGTH: 411 amino acids
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                     TOPOLOGY:
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                                                                                                                                 (516) 742-4366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              United States
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US-08-902-853-7
; Sequence 7, Application US/08902853
; Patent No. 5945330
RESULT 6
PCT-US95-06725-2
; Sequence 2, Application PC/TUS9506725
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/902,853
FILING DATE: Herewith
CLASSIFICATION: 7
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                      Query Match
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APPLICANT:
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APPLICANT: Lal, Preeti
TITLE OF INVENTION: HUMAN LONGEVITY-ASSURANCE PROTEIN HOMOLOGS
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
LIBRARY: GenBa
CLONE: 541568
                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 411 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Billings, Lucy J.
REGISTATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                              311 VEFWI 315
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                                                                                                                                                       Local Similarity
nes 4; Conserv
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CITY: Palo Alto
STATE: CA
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                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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                                                                                                                          1 IFFWI 5
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Corley, Neil C.
Shah, Purvi
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Pred. No. 3.7e+02;
                                                                                                                                                                         Score 30; DB 2;
Pred. No. 3.7e+02;
                                                                                                                                                       Mismatches
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                                                                                                                                                                                      DB 2;
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US-08-844-064-7
; Sequence 7, Application US/08844064
; Patent No. 5747314
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TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEFAX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 411 mino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
SOFTWARE: FASTSEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/844,064
FILING DATE: 18-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/253,875 & 08/336,031
FILING DATE: 03-JUN-1994 & 08-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,346
                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline
                                                                                                                                                                                                                                                                                                    APPLICANT: Lawlor, I
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                 STREET: 709 Swedeland CITY: King of Prussia STATE: PA
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                                                                                                                                                                                                                                             ADDRESSEE: SMILINIAL STREET: 709 Swedeland
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
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                                                                                                                                                                                 ZIP:
                                                                                                                                                                                                COUNTRY:
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19406-0939
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Pred. No. 3.7e+02;
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; MOLECULE TYPE: US-09-009-433-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/09009433
Patent No. 6087142
GENERAL INFORMATION:
APPLICANT: Lawlor, Elizabeth
TITLE OF INVENTION: No. 6087142el Compounds
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKilne Beecham Corporation
                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/844,064
APPLICATION NUMBER: 08/844,064
FILING DATE: 18-APR-1997
APPLICATION NUMBER: 9607991.8
FILING DATE: 18-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           uery Match
                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                           NAME: Gimmi Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P31458-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         279 IFFWV 283
                                   TYPE: amino acid
STRANDEDNESS: Si
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 709 Swederand CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 19406-0939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                         LENGTH:
                                                                                                                                                             TELEFAX:
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                                                                                         amino acids
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Query Match
Best Local Similarity
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; MOLECULE TYPE: protein
US-08-068-392-2
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US-08-068-392-2
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                                                                                                                                                                 Sequence 2, Application US/08396988 Patent No. 6204043
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Best Local Similarity
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                                                                                                   GENERAL INFORMATION:
APPLICANT: Shapiro, Steven M.
TITLE OF INVENTION: Human Mac
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS LENGTH: 470 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Meyer, Scott J.
REGISTRATION NUMBER: 25275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)694-3117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Shapiro, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                            305 FFWLK 309
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                                          STREET: 8 CITY: St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 199305 CLASSIFICATION: 435
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COMPUTER: IBM PC compatible
OPERATING.SYSTEM: PC-DOS/MS-DOS
                            STATE:
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COUNTRY: USA
ZIP: 63167
                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE:
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                                                                        ADDRESSEE:
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: Missouri
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                            Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                           470 amino acids
                                                        800 N. Lindbergh Blvd
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                                                                                                                                                                                                                                                                                                                        Conservative
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                                            Louis
                                                                       Scott J.
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                                                                        Meyer, Monsanto Co., A3SM
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Pred. No. 4.2e+02;
Pred. No. 4.2e+02;
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Pred. No. 3.8e+02;
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; SOFTWARE: FastSEQ for W:

; SEQ ID NO 26

; LENGTH: 470

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-391-104-26
RESULT 12
US-08-475-894-2
; Sequence 2, Application US/08475894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
US-09-391-104-26
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; MOLECULE TYPE:
US-08-396-988-2
                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 26, Application US/09391104 Patent No. 6399371
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Best Local Similarity
                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Falduto, Michael T.
APPLICANT: Magnuson, Scott R.
APPLICANT: Morgan, Douglas W.
TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
TITLE OF INVENTION: OF USING SAME
TITLE REFERENCE: 6073 US. P1
CURRENT APPLICATION NUMBER: US/09/391,104
CURRENT FILING DATE: 1999-09-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 01-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/068,392
FILING DATE: 28-MAY-1993
ATTORNEY,AGENT INFORMATION:
NAME: Meyer, Scott J.
REGISTRATION NUMBER: 25275
REFERENCE/DOCKET NUMBER: .07-24(1240)
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1997-
                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                 305 FFWLK 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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(314)694-5435
770 TD NO: 2:
                                                                                                                                              Conservative
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BER: US 08/814,394
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80.0%;
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                                                                                                                                            Score 30; DB Pred. No. 4.2e.
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .07-24 (12406)A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 30; DB 4;
Pred. No. 4.2e+02;
                                                                                                                                           1.2e+02;
0;
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US-08-484-710-2

; Sequence 2, Application US/08484710

; Patent No. 5656438
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TELEPHONE: (617)227-7400
TELEPAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                   ZIF: 02109-1875

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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NAME: LOUIS MYETS
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: BG:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
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LENGTH: 553 amino acid
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TITLE OF INVENTION: THE CAIP-LIKE GENE FAMILY
                                       ATTORNEY/AGENT INFORMATION:
NAME: Louis Myers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Yen-ming Hsu
TITLE OF INVENTION: THE CAIP-LIKE GENE FAMILY
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CITY: Boston
                                                                                                         FILING DATE: CLASSIFICATION:
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NAME: Louis Myers
REGISTRATION NUMBER:
                                                                                                                                                                                            APPLICATION NUMBER:
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internal
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Pred. No. 4.9e+02;
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Gaps

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REFERENCE/DOCKET NUMBER: BG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941

BGP-190

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RESULT 15
US-08-474-697-2
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US-08-484-709-2
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Best Local Similarity 80...
Conservative
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Best Local Similarity
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Patent NO. 5837844
GENERAL INFORMATION:
APPLICANT: YEN-Ming Hsu
TITLE OF INVENTION: THE CAIP-LIKE GENE FAMILY
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                   TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                        TOPOLOGY: 11r
MOLECULE TYPE:
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,709
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
FORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: LOUIS MYERS
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: BG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
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LENGTH: 553 amino acids
TYPE: amino acid
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CITY: Boston
STATE: Massac
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--- NO: 2:
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Pred. No. 4.9e+02;
1; Mismatches (
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                                                                                                                                           Score 30; DB 2;
Pred. No. 4.9e+02;
                                                                                                                               Mismatches
                                                                                                                                                        Length 553;
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MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-474-697-2
Search completed: January
Job time : 10 secs
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (617)227-5941 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LOUIS MYETS
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: BGP-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/474,697
                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Yen-Ming Hsu
TITLE OF INVENTION: THE CAIP-LIKE GENE FAMILY
                                                                           68 IFFWV 72
                                                                                                                                                                                                                                                                                   TOPOLOGY:
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CITY: Boston
                                                                                                            1 IFFWI 5
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                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                 linear
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Pred. No. 4.9e+02;
1; Mismatches 0;
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Database :
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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                                                                                                                                                                                                                                                                                                                                                                                                            length: 0
length: 2000000000
          January 3, 2003, 15:32:11; Search time 4.77273 Seconds (without alignments) 23.825 Million cell updates/sec
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                                                                                                                                                                                                                                                                                         Published_Applications_AA: *
: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

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/cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

No.	Score	Match	Length	BB	ID	Description
1	35	97.2	487	ٰ و	US-09-738-626-6481	Sequence 6481,
2	31	86.1	53	10	US-09-864-761-40676	Sequence 40676,
ω	31	86.1	58	10	US-09-867-550-866	Sequence 866,
4	31	86.1	79	10	US-09-205-658-325	Sequence 325
ъ	31	86.1	951	10	US-09-815-242-10465	
O	31	86.1	951	10	US-09-815-242-13853	
7	31	86.1	1256	10	US-09-935-291A-6	
œ	30	83.3	137	10	US-09-867-550-832	
9	30	83.3	312	10	US-09-393-634-51	51
10	30	83.3	445	ဖ	US-09-992-598-177	Sequence 177, App
11	30	83.3	445	9	US-09-989-293A-177	177,
12	30	83.3	445	ø	US-10-063-547-32	
13	30	83.3	445	φ	US-09-989-735-177	177
14	30	83.3	445	9	US-09-990-444-177	177,
15	30	83.3	445	9	US-09-989-730-177 •	Sequence 177, App
16	30	83.3	445	9	US-09-990-436-177	177
17	30	83.3	445	9	US-09-991-181-177	
18	30	83.3	445	9	US-09-993-687-177	
19	30	83.3	445	10	115-00-000-700-177	Secuence 177 App

45	44	43	42	41	40	.39	38	37	36	35 5	34	ω	32	31	30	29	28	27	26	25	24	23	22	21	20
29	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30
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34	954	950	883	883	880	879	877	876	810	473	470	470	445	445	445	445	445	445	445	445	445	445	445	445	445
10	10	10	10	10	10	10	10	10	10	10	10	9	12	12	10	10	10	10	10	10	10	10	10	10	10
US-09-864-761-49024	242-	US-09-815-242-11961	-242-	-242-	-242-	-242	US-09-815-242-4876	US-09-815-242-13003	US-09-815-242-12636	US-09-925-301-1217	US-09-801-196-23	US-09-920-455-219	US-10-052-586-148	•		-456-	US-09-993-604-177		- 1		US-09-989-732-177	-989-731-	US-09-989-727-177	ò	US-09-989-723-177
	Sequence 11238, A		13684,		10675,	Sequence 5312, Ap	4876,	Sequence 13003, A	12636	1217		219,	148,	32,	177,	177,	Sequence 177, App	177,	177,	177	177	177	177	Sequence 177, App	

## ALIGNMENTS

US-09-738-626-6481

Sequence 6481, Application US/09738626 Publication No. US20020197605A1

GENERAL INFORMATION:

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                                                                                                                                ; TYPE: PRT ; ORGANISM: Corynebacterium glutamicum US-09-738-626-6481
                                                                                                                                                                                                                                                                                APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
FULE REFERENCE: 249-125
CURRENT APPLICATION UMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
                                                                                                                                                                               NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN VER. 3.0
SEQ ID NO 6481
LENGTH: 487
                                                                Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: JP 00/280988 PRIOR FILING DATE: 2000-08-03
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412 VFFWIK 417
                               1 IFFWIK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATEISHI, NAOKO
SENOH, AKIHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OCHIAI, KEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                     IKEDA, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YOKOI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAYASHI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIZOGUCHI, HIROSHI
                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HARUHIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MIKIRO
                                                                               97.2%;
83.3%;
                                                                 1;
                                                                               Score 35; Pred. No.
                                                                Mismatches
                                                                                   . 33;
                                                                                                  9.
                                                                                             Length 487;
                                                                 Indels
                                                                 0,
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Query Match
Best Local Similarity
""+ches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
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CURRENT FILING DATE: 2001-05-23
                                                                                                                                  OTHER INFORMATION: MAP TO ACO15473.3

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.9

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.6

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.6

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.4

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.4

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.0

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.1

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/207,456 PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/180,312 PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: Acomica-X-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ID NO 40676
ENGTH: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US (FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US01/00667 FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/US01/00664 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 2000-09-27 APPLICATION NUMBER: PCT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US01/00662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US01/00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US01/00665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 2001-01-30
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5. US20020048763A1
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Chen, Wensheng
                      86.1%; S ilarity 100.0%; Conservative 0;
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                      Score 31; DB; Pred. No. 22; 0; Mismatches
                                                                                                                                       IN BONE MARROW, SIGNAL = 4.1
HIT: 002791, EVALUE 1.00e-25
HIT: AW389879.1, EVALUE 2.00e-24
                                                                  10;
                      0;
                                                               Length 53
                        Indels
                      0;
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Best Local
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                      61 IFFWYK
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US-09-205-658-325

US-09-205-658-325

; Sequence 325, Application US/09205658

; Patent No. US20010029617A1

; GENERAL INFORMATION:
Query Match
Best Local Similarity
""" hes 5; Conserv
                                                                                         ; TYPE: PRT
; ORGANISM: Homo sapiens or Caenorhabditis elegans
US-09-205-658-325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens US-09-867-550-866
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US-09-867-550-866
                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 325
LENGTH: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows SEQ ID NO 866
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                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ruvkun, Gary
APPLICANT: 099, Scott
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
FILE REFERENCE: 00786/351004
CURRENT APPLICATION NUMBER: US/09/205,658
CURRENT FILING DATE: 1998-12-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Topper, James
TITLE OF INVENTION: No. US20020082206Alel Polynucleotides from Atherogenic Cells
TITLE OF INVENTION: Thereby
FILE REFERENCE: 21402-013 (Cura-373)
                                                                                                                                                                                                                        EARLIER APPLICATION NUMBER: US98/10080 EARLIER FILING DATE: 1998-05-15
                                                                                                                                                                                                                                                             EARLIER APPLICATION NUMBER: 08/857,076
EARLIER FILING DATE: 1997-05-15
EARLIER APPLICATION NUMBER: 08/888,534
EARLIER FILING DATE: 1997-07-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Thereby FILE REFERENCE: 21402-013 (Cura-313) CURRENT APPLICATION NUMBER: US/09/867,550 CURRENT FILING DATE: 2001-09-20 PRIOR APPLICATION NUMBER: USSN 60/208,427 PRIOR FILING DATE: 2000-05-30
                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Leach, Martin D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 2125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42 FFWVK 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
les 4; Conserv
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Conley, Pamela
Law, Debbie
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                   Conservative
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                                   86.1%;
83.3%;
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80.0%;
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Pred. No.
                                     Score 31;
Pred. No.
                   Mismatches
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                                     DB
31;
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24;
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                 1;
                                                  Length 79;
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                 Indels
                 0;
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                 Gaps
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                 0
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US-09-815-242-10465

Sequence 10465, Application US/09815242 Patent No. US20020061569A1

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Query Match
Best Local Similarity
Thehes 5; Conserve
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US-09-815-242-10465
                                                                                                                                                                                                                                                                                                                                                                                 US-09-815-242-13853
                                                                                                                                                                                                                                                                                                                                            Sequence 13853, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 10465
LENGTH: 951
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                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
                                                                                                                    APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                           APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L. APPLICANT: Zyskind, Judith W.
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
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                                                                                                                                                                                                                                            APPLICANT: Wall, Daniel
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PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269, 308
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PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
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PRIOR FILING DATE: 2000-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE:
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Zyskind, Judith W.
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Xu, H. Howard
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                                                                                                                                            of Essential Genes
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2.9e+02;
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; LENGTH: 1256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-291A-6
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Best Local Similarity
~~+~hes 5; Conserva
                                                                                                     GENERAL INFORMATION:
APPLICANT: Leach, Martin D.
APPLICANT: Mehraban, Fuad,
APPLICANT: Conley, Pamela
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Best Local Similarity
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APPLICANT: Chun, Miyoung
TITLE OF INVENTION: 49937, 49931, AND 49933, NOVEL HUMAN TRANSPORTER
TITLE OF INVENTION: FAMILY MEMBERS AND USES THEREOF
FILE REFERENCE: MNI-184
CURRENT APPLICATION NUMBER: US/09/935,291A
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: 60/226,504
PRIOR FILING DATE: 2000-08-21
PRIOR FILING DATE: 2000-08-21
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PRIOR FILING DATE: 2000-11-30
NUMBER OF SEQ ID NOS: 52
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PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
DRIOR FILING DATE: 2000-11-27
APPLICANT: Topper, James
TITLE OF INVENTION: No. US20020082206A1el Polynucleotides from Atherogenic Cells
TITLE OF INVENTION: Thereby
FILE REFERENCE: 21402-013 (Cura-313)
                                                                 APPLICANT:
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PRIOR FILING DATE: 2000-12-2
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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APPLICANT:

Godowski, Paul J.

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US-09-992-598-177; Sequence 177, Application US/09992598
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US-09-867-550-832
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                                                                                                                                                        Patent No. US20020160384A1
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Best Local Similarity
                               APPLICANT:
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APPLICANT:
                                                                                       APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                            APPLICANT:
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                                                             APPLICANT:
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ORGANISM: Homo sapiens
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nes 4; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The Regents of the University of California The Government of the United States of America as represented by the Secretary of the Department of Health and Human Services
Gerber, Hanspeter
Gerritsen, Mary E
                              Ferrara, Napoleone
Fong, Sherman
                                                             Eaton, Dan L.
                                                                          Desnoyers, Luc
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Pred. No.
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APPLICANT:
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PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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OR APPLICATION NUMBER: 60/066770
OR FILING DATE: 1997-11-24
OR APPLICATION NUMBER: 60/075945
OR FILING DATE: 1998-02-25
OR APPLICATION NUMBER: 60/078910
OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/083322
                                                                    APPLICATION NUMBER: FILING DATE: 1998-0
                                                                                                      APPLICATION NUMBER: 60/088202 FILING DATE: 1998-06-05
                               APPLICATION NUMBER: 60/088217 FILING DATE: 1998-06-05
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                                                                                                                                                                                                                                                                    FILING DATE: 1998-0 APPLICATION NUMBER:
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088025
FILING DATE: 1998-06-04
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                                                                                                                                           FILING DATE:
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DR FILING DATE: 1998-06-23
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RESULT 11
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OR FILING DATE: 1998-07-02
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DR FILING DATE: 1998-07-01
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DR FILING DATE: 1998-07-02
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||FFWV 137
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            Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Kljavin, Ivar J.
                                                                                                                                                                                        Ashkenazi, Avi J
Baker, Kevin P.
                                                                                                                   Fong, Sherman
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                                                                                                                                               Eaton, Dan L.
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Napier, Mary A.
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APPLICANT

Paoni, Nicholas

Pan, James

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TITLE OF INVENTION: Secreted and Transmembran
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US-10-063-547-32
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,547
CURRENT FILING DATE: 2002-05-02
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APPLICANT: Eaton, Dan L.
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US-09-989-735-177; Sequence 177, A; Publication No.
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PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/989,735
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ashkenazi, Avi J. APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/065311 PRIOR FILING DATE: 1997-11-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730P1C61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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FILING DATE: 1998-06-03
APPLICATION NUMBER: 60/0
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/0
                                                                                                                                                                                FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/087106
FILING DATE: 1998-05-28
                                                                 FILING DATE: 1998-00 APPLICATION NUMBER:
                                                                               APPLICATION NUMBER: 60/087759
FILING DATE: 1998-06-02
                                                                                                                                APPLICATION NUMBER: 60/087609
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APPLICATION NUMBER: 60/084600
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Williams,
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Stewart, Timothy A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumas, Daniel
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NUMBER: 60/088025
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60/088202 .60/088167

60/088212

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60/088326 60/088033

APPLICATION NUMBER: 60/ FILING DATE: 1998-06-04

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1998-06-04 1998-06-04

60/088028 60/088026

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APPLICATION NUMBER: 60/088742 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/0 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088734 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/0 FILING DATE: 1998-06-09

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OR APPLICATION NUMBER: 60/091544
OR FILING DATE: 1998-07-01
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OR APPLICATION NUMBER: 60/091626
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091633
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091978
OR FILING DATE: 1998-07-07
OR APPLICATION NUMBER: 60/091978
OR FILING DATE: 1998-07-07
OR APPLICATION NUMBER: 60/091982
OR APPLICATION NUMBER: 60/091982
OR APPLICATION NUMBER: 60/092182
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DR APPLICATION NUMBER: 60/090472

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PR APPLICATION NUMBER: 60/090252
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APPLICATION NUMBER: 60/090694
APPLICATE: 1998-06-25
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1998-06-16

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NUMBER: 60/089532 1998-06-17

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NUMBER: 60/088858 1998-06-11 1998-06-10

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DR FILING DATE: 1998-06-17
DR APPLICATION NUMBER: 60/089538
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NUMBER: 50, NUMBER: 50, TE: 1998-06-19 TYPER: 60/089952

NUMBER: 60/089947 1998-06-19

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CURRENT FILING DATE: 2001-11-14
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TITLE OF INVENTION: Secreted and
TITLE OF INVENTION: Acids Encodi
FILE REFERENCE: P2730P1C19
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R APPLICATION NUMBER: 60/087607
DR FILING DATE: 1998-06-02
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Baker, Kevin P.
Botstein, David
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Gerritsen, Mary E
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RESULT 15
US-09-989-730-177
; Sequence 177, Application US/09989730
; Publication No. US20020197674A1
; GENERAL INFORMATION:
; APPLICANT: AShkenazi, Avi, J.
; APPLICANT: Baker, Kevin P.
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R FILING DATE: 1998-06-26

R APPLICATION NUMBER: 60/090863

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DR APPLICATION NUMBER: 60/091360

DR FILING DATE: 1998-07-01

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DR FILING DATE: 1998-06-25
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APPLICATION NUMBER: 60/092182
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PRIOR APPLICATION NUMBER: 60/049787
PRIOR TILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-11-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
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PRIOR PILING DATE: 1997-11-13
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PRIOR APPLICATION NUMBER: 60/06770
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PRIOR APPLICATION NUMBER: 60/075945
PRIOR APPLICATION NUMBER: 60/078910
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